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GenCore version 4.5
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OM protein - protein search, using sw model

Run on: July 26, 2000, 13:15:21 ; Search time 33.21 Seconds

(without alignments)
99.138 Million cell updates/sec

Title: US-09-203-768a-2

Perfect score: 1 MKHLMEFLLVAAPRMVL5Q.....ARPRYFDYMGSTLVTS 139

Sequence:

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 188963 seqs, 23686106 residues

Number of hits satisfying chosen parameters: 188963

Minimum DB seq length: 0
Maximum DB seq length: 1000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database: A_Geneseq_36:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match Length | ID | Description |
|------------|-------|--------------------|-----|----------------------|
| 1 | 622 | 83.2 | 116 | Human immunoglobulin |
| 2 | 575.5 | 76.9 | 472 | Anti-rhesus D reco |
| 3 | 560.5 | 74.9 | 136 | Immunoglobulin R6 |
| 4 | 558.5 | 74.7 | 123 | Anti-rhesus D mono |
| 5 | 558.5 | 74.7 | 142 | F105 rearranged va |
| 6 | 552 | 73.8 | 128 | Anti-human Rhd FOM |
| 7 | 550 | 73.5 | 116 | Vh 71-4. DNA segme |
| 8 | 550 | 73.5 | 116 | Human immunoglobulin |
| 9 | 541.5 | 72.4 | 476 | Primate anti-hu |
| 10 | 541.5 | 72.4 | 476 | Macaque primate |
| 11 | 539 | 72.1 | 118 | Human immunoglobulin |
| 12 | 539 | 72.1 | 475 | Monoclonal antibody |
| 13 | 538 | 71.9 | 116 | Human immunoglobulin |
| 14 | 536.5 | 71.7 | 140 | Anti-CD4 cynomolg |
| 15 | 536.5 | 71.7 | 140 | Monoclonal antibody |
| 16 | 536.5 | 71.7 | 141 | Anti-CD4 VH peptid |
| 17 | 536.5 | 71.7 | 467 | Human gamma-4P he |
| 18 | 536.5 | 71.7 | 467 | Human gamma-4 heav |
| 19 | 536.5 | 71.7 | 467 | Human gamma-4E hea |
| 20 | 536 | 71.7 | 141 | Anti-human CD23 6G |
| 21 | 533.5 | 71.2 | 139 | Monkey anti-CD4 he |
| 22 | 533.5 | 71.2 | 139 | Monkey anti-human |
| 23 | 533.5 | 71.2 | 139 | Anti-CD4 antibody |
| 24 | 530.5 | 70.9 | 134 | Sequence of the VH |
| 25 | 530.5 | 70.9 | 134 | Monoclonal antibody |
| 26 | 530.5 | 70.9 | 134 | Monoclonal antibody |
| 27 | 529.5 | 70.8 | 121 | Anti-human Rhd FOM |
| 28 | 529.5 | 70.8 | 476 | Primate anti-hu |
| 29 | 529.5 | 70.8 | 476 | Macaque primate |
| 30 | 527 | 70.5 | 118 | Human immunoglobulin |
| 31 | 527 | 70.5 | 125 | Variable region of |
| 32 | 526.5 | 70.4 | 139 | Anti-CD4 antibody |
| 33 | 521 | 69.7 | 118 | Human immunoglobulin |

| | | | | | |
|----|-------|------|-----|---|---------|
| 34 | 515.5 | 68.9 | 528 | 1 | R52952 |
| 35 | 514 | 68.7 | 120 | 1 | R66343 |
| 36 | 508 | 67.9 | 119 | 1 | R54799 |
| 37 | 507 | 67.8 | 107 | 1 | R12857 |
| 38 | 501 | 67.0 | 244 | 1 | R106718 |
| 39 | 499.5 | 66.8 | 117 | 1 | R66330 |
| 40 | 495.5 | 66.2 | 119 | 1 | R27554 |
| 41 | 494 | 66.0 | 124 | 1 | R12268 |
| 42 | 493.5 | 66.0 | 117 | 1 | R38659 |
| 43 | 484 | 64.7 | 97 | 1 | P50100 |
| 44 | 476 | 63.6 | 124 | 1 | W06474 |
| 45 | 471 | 63.0 | 116 | 1 | R38670 |

ALIGNMENTS

| | |
|---|---|
| RESULT 1 | |
| ID R66324 | R66324 standard; Protein; 116 AA. |
| AC R66324 | 03-AUG-1995 (first entry) |
| DE Human immunoglobulin variable heavy chain #30. | |
| PR Primer; PCR; amplify; human; immunoglobulin; variable; heavy chain; | |
| KW cosmid; placenta; vector; pJB81; E.coli; mammalian. | |
| OS Homo sapiens. | |
| PN W09426895-A. | |
| PD 24-NOV-1994 | |
| PE 10-MAY-1993; J00603. | |
| PR 10-MAY-1993; W0-J00603. | |
| PA (N15B) JAPAN TOBACCO INC. | |
| PI WPI: 95-006791/01. | |
| DR N-PSDB: Q78972. | |
| PT DNA fragment comprising human immunoglobulin Vh genes - for the | |
| PS production of human immunoglobulin in mammalian hosts | |
| CC Protein sequences (R66295-51) are novel human immunoglobulin heavy chain | |
| CC sequences encoded by novel isolated genes. The genes (Q78939-79002) were | |
| CC isolated and cloned from a series of cosmid constructs: Y202; Y103; Y21; | |
| CC Y6/Y24; 3-31; M84; M18 and M31, by PCR amplification using primers | |
| CC Q78917-38. The genes are subdivided into 5 families of Vh genes. The | |
| CC fragments cover a region of 800 kb. The DNA fragments were isolated from | |
| CC high molecular weight DNA from human placenta. The DNA was partially | |
| CC digested with TaqI restriction enzyme. The fragments were separated by | |
| CC gel electrophoresis and 35-45 kb fractions were collected. The fragments | |
| CC were ligated with clai-digested cosmid vector pJB81. The ligation | |
| CC products were in vitro packed and infected into E.coli 490A. The | |
| CC fragments were then subcloned by colony hybridisation. The Vh genes and | |
| CC the DNA fragments encoding them are useful in producing human | |
| CC immunoglobulin in mammalian hosts. | |
| CC Sequence 116 AA; | |
| QY | 1 MKHLMEFLLVAAPRMVL5QVLOQMGAGLKPSTSLTCVAVYGSFGYWSIRPP 60 |
| DB | 1 MKHLMEFLLVAAPRMVL5QVLOQMGAGLKPSTSLTCVAVYGSFGYWSIRPP 60 |
| QY | 61 GKGLEWIGELINSGSTNPNPSIKSRVTISVDTSKNQSFILKSSVTAADTAVYYCAR 116 |
| DB | 61 GKGLEWIGELINSGSTNPNPSIKSRVTISVDTSKNQSFILKSSVTAADTAVYYCAR 116 |
| RESULT 2 | |
| ID R93166 | R93166 standard; Protein; 472 AA. |
| AC R93166 | 30-OCT-1996 (first entry) |
| DE Anti-rhesus D recombinant antibody D7C2 heavy chain. | |

Human monoclonal antibody; immunoglobulin isotype IgM; agglutination;
 rhesus positive; rhesus negative; haemolysis; gamma 1 heavy chain;
 variable region; insect host cell; baculovirus; recombinant production.
 OS Homo sapiens.
 OS Synthetic.
 FT Key Location/Qualifiers
 FT peptide 1..19
 FT /label="signal_peptide
 FT /note="mouse VH signal peptide sequence encoded by
 FT synthetic linker"
 FT 20..472
 FT protein /label="heavy_chain
 FT /note="human gamma 1 chain constant region
 FT and the variable region from anti-rhesus D
 FT antibody D7C2"
 FT FR2724182-A1.
 PD 08-MAR-1996.
 PD 02-SEP-1994; FR-010566.
 PE 02-SEP-1994; FR-010566.
 (INSP) INST PASTEUR.
 PA (PROT-) PROTEIN PERFORMANCE.
 PI Chaabih H, Edelman L, Kaczorek M, Margalit C;
 DR WPI; 96-162018/17.
 DR N-PSDB; T26889.
 PT Recombinant anti-rhesus D monoclonal antibody - expressed by
 PT baculovirus-transformed insect cells and useful for preventing
 PT haemolysis in new-born babies
 PS Example 2; Page 35-37; 46pp; French.
 CC The human monoclonal antibody D7C2, of isotype IgM, recognises a
 CC 30-32 kD polypeptide on the membrane of rhesus positive red blood
 CC cells. The antibody agglutinates rhesus positive cells but not
 CC rhesus negative cells and is useful diagnostically and also for
 CC preventing haemolysis in new-born rhesus positive babies.
 CC Recombinant IgM-D7C2 can be produced by insect cells which have
 CC been transformed by a baculoviral vector comprising a D7C2
 CC expression cassette. The present sequence is that of a recombinant
 CC IgM-D7C2 heavy chain fused downstream of a mouse VH signal peptide.
 SO Sequence 472 AA;

Query Match 76.98; Score 575.5; DB 1; Length 472;
 Best Local Similarity 85.28; Pred. No. 1.1e-40;
 Matches 115; Conservative 3; Mismatches 14; Indels 3; Gaps 2;
 QY 8 LLLAARRWVLSOYQLOQMGAGLKPSETSLTCAVYGSFGSYWMSIRPPKGLWMI 67
 D 8 LFLVATRGVHSQVQLQDGMGAGLKPSETSLTCTVYGSGFSGYWMSIRPPKGLWMI 67
 QY 68 GEINHSSTNNPSPSLKSRVTISVDTSKNQPSLKLSTVTAADTAAYVCAR--EIAAPH-R 124
 D 68 GEINHSSTNNPSPSLKSRVTISVDTSKNQPSLKLSTVTAADTAAYVCARAEYKMKYIGD 127
 QY 125 YEDYWGQGLTVTVSS 139
 D 128 WFDPMGGGTIVTVSS 142
 RESULT 3
 W24536
 ID W24536 standard; Protein; 136 AA.
 AC W24536;
 DT 09-OCT-1997 (first entry)
 DE Immunoglobulin rB6B7 heavy chain variable region.
 KW Immunoglobulin: variable region; heavy chain; thyrotropin receptor;
 KW thyroid stimulating activity; light chain; Basedow's disease; antibody;
 KW peripheral blood lymphocyte.
 OS Homo sapiens.
 FT Key Location/Qualifiers
 FT peptide 1..19
 FT /note="signal peptide"
 FT 20..136
 FT protein
 PD J09140386-A.
 PD 03-JUN-1997.

PE 22-NOV-1995; 328235.
 PR 22-NOV-1995; JP-328235.
 PA (EIKE) EIKEN KAGAKU KK.
 DR WPI; 97-344899/32.
 DR N-PSDB; T79919.
 PT Antibody containing immunoglobulin heavy chain mutation - with
 PT thyroid function stimulating activity
 PS Claim 31; Page 14-15; 18pp; Japanese.
 CC W24536-W24539 represent the immunoglobulin heavy and light chain variable
 CC regions isolated from peripheral blood lymphocyte strains. These
 CC sequences were isolated from the B6B7 and 101-2 strains of peripheral
 CC blood lymphocytes of a Basedow's disease patient. These sequences are
 CC replaced, deleted or inserted into an antibody, to create the antibodies
 CC of the invention. The antibodies of the invention have thyroid function
 CC stimulating activity, and act by combining with thyrotropin receptor. The
 CC antibody can be used in a method to detect autoantibodies which have
 CC thyroid function stimulating activity.
 SO Sequence 136 AA;

Query Match 74.98; Score 560.5; DB 1; Length 136;
 Best Local Similarity 81.68; Pred. No. 5.7e-40;
 Matches 111; Conservative 4; Mismatches 18; Indels 3; Gaps 2;
 QY 1 MKHMFLLVAAARWVLSOYQLOQMGAGLKPSETSLTCAVYGSFGSYWMSIRPP 60
 D 1 MKHMFLLVAAARWVLSOYQLOQMGAGLKPSETSLTCTVSGDSSISYWSIRPP 60
 QY 61 GKGLEWIGEINHSSTNNPSPSLKSRVTISVDTSKNQPSLKLSTVTAADTAAYVCAR-- 118
 D 61 GKGLEWIGEINHSSTNNPSPSLKSRVTISVDTSKNQPSLKLSTVTAADTAAYVCARERG 120
 QY 119 AARPHRY-FDYWGQGT 133
 D 121 GLRDFAYGMDVWGQGT 136

RESULT 4
 W03757
 ID W03757 standard; Protein; 123 AA.
 AC W03757;
 DT 29-OCT-1996 (first entry)
 DE Anti-rhesus D monoclonal antibody D7C2 heavy chain V region.
 KW Human monoclonal antibody; immunoglobulin isotype IgM; agglutination;
 KW rhesus positive; rhesus negative; haemolysis; heavy chain;
 KW variable region; insect host cell; baculovirus; recombinant production.
 OS Homo sapiens.
 FT Key Location/Qualifiers
 FT region 29..35
 FT /label="CDR1
 FT /note="complementarity determining region"
 FT region 50..65
 FT /label="CDR2
 FT /note="complementarity determining region"
 FT region 98..112
 FT /label="CDR3
 FT /note="complementarity determining region"
 FT FR2724182-A1.
 PD 08-MAR-1996.
 PD 02-SEP-1994; FR-010566.
 PE 02-SEP-1994; FR-010566.
 PA (INSP) INST PASTEUR.
 PA (PROT-) PROTEIN PERFORMANCE.
 PI Chaabih H, Edelman L, Kaczorek M, Margalit C;
 DR WPI; 96-162018/17.
 DR N-PSDB; T26870.
 PT Recombinant anti-rhesus D monoclonal antibody - expressed by
 PT baculovirus-transformed insect cells and useful for preventing
 PT haemolysis in new-born babies
 PS Example 1; Page 32; 46pp; French.
 CC The human monoclonal antibody D7C2, of isotype IgM, recognises a
 CC 30-32 kD polypeptide on the membrane of rhesus positive red blood
 CC cells. The antibody agglutinates rhesus positive cells but not

KW Monoclonal antibody; Mab; envelope; glycoprotein; gp120; HIV; AIDS;
 KW CD4; receptor; hybridoma; polymerase chain reaction; PCR; heavy; light;
 KW chain; epitope; immune deficiency.
 OS Homo sapiens.
 FH Location/Qualifiers
 FT peptide 1..19
 FT /label= sig_peptide
 FT 20..116
 FT /label= mat_protein
 FT region 49..54
 FT /label= CDR1
 FT region 69..84
 FT /label= CDR2
 PN WO9312232-A.
 PD 24-JUN-1993.
 PF 10-DEC-1992; U10928.
 PR 10-DEC-1991; US-804652.
 PA (DAND) DANA FARBER CANCER INST INC.
 PA (NEW-) NEW ENGLAND DEACONNESS HOSPITAL CORP.
 P Haseltine WA, Marasco WA, Posner MR, Sodroski JG;
 P WPI: 93-214174/26.
 DR N-PSDB; Q42697.
 PT DNA segments encoding monoclonal antibody - which binds to gp120
 PT and neutralises HIV, for treating AIDS, and for diagnosing and
 PT monitoring HIV infection
 PS Disclosure: Page 64; 109pp; English.
 CC The nucleotide sequence of rearranged F105 Vh (Q42698) was compared
 CC to two monoclonal antibodies (Ab26 - Q42702) and 268-D - Q42703),
 CC which by nucleotide sequence analysis, appear to be a rearranged
 CC Vh 71-4 gene (Q42697).
 CC Ab26 (Q42702) was derived from CD5+ B cells of a healthy donor and
 CC represents a naturally occurring polyclonal antibody which binds to
 CC many antigens. Ab26 shares greatest sequence similarity with germline
 CC Vh 71-4.
 SQ Sequence 116 AA;

Query Match 73.5%; Score 550; DB 1; Length 116;
 Best Local Similarity 90.5%; Pred. No. 3.6e-39;
 Matches 105; Conservative 3; Mismatches 8; Indels 0; Gaps 0;

QY 1 MKHLWFFLLVAPRWVLSQVQLQDQAGLLKPKSETLSITCAVYGGSGFYWSWIRPP 60
 DB 1 MKHLWFFLLVAPRWVLSQVQLQDQAGLLKPKSETLSITCAVYGGSGFYWSWIRPP 60

QY 61 GKLEWIGELNHSSTNYPNLSKRVITISVDTSKNOFSLKLSVTADTAAYVCAR 116
 DB 61 GKLEWIGELNHSSTNYPNLSKRVITISVDTSKNOFSLKLSVTADTAAYVCAR 116

RESULT 8
 ID R66346 standard; Protein: 116 AA.
 AC R66346;
 DT 04-AUG-1995 (first entry)
 DE Human immunoglobulin variable heavy chain #52.
 KW Primer; PCR; amplify; human; immunoglobulin; variable; heavy chain;
 KW cosmid; placenta; vector; pJB81; E.coli; mammalian.
 OS Homo sapiens.
 PN WO9426895-A.
 PD 24-NOV-1994.
 PF 10-MAY-1993; J00603.
 PR 10-MAY-1993; WO-J00603.
 PA (NIBS) JAPAN TOBACCO INC.
 PA Honjo T, Matsuda F;
 PI WPI: 95-006791/01.
 DR N-PSDB; Q78997.
 PT DNA fragment comprising human immunoglobulin Vh genes - for the
 PT production of human immunoglobulin in mammalian hosts
 PS Disclosure: Page 107-108; 130pp; Japanese.
 CC Protein sequences (R66295-51) are novel human immunoglobulin heavy chain
 CC sequences encoded by novel isolated genes. The genes (Q78939-79002) were
 CC isolated and cloned from a series of cosmid constructs: Y202; Y103; Y21;

CC Y6;Y24; 3-31; M84; M18 and M31, by PCR amplification using primers
 CC Q78917-38. The genes are subdivided into 5 families of Vh genes. The
 CC fragments cover a region of 800 kb. The DNA fragments were isolated from
 CC high molecular weight DNA from human placenta. The DNA was partially
 CC digested with RsaI restriction enzyme. The fragments were separated by
 CC gel electrophoresis and 35-45 kb fragments were collected. The fragments
 CC were ligated with ClaI-digested cosmid vector pJB81. The ligation
 CC products were in vitro packed and infected into E.coli 430A. The
 CC fragments were then subcloned by colony hybridisation. The Vh genes and
 CC the DNA fragments encoding them are useful in producing human
 CC immunoglobulin in mammalian hosts.
 SQ Sequence 116 AA;

Query Match 73.5%; Score 550; DB 1; Length 116;
 Best Local Similarity 90.5%; Pred. No. 3.6e-39;
 Matches 105; Conservative 3; Mismatches 8; Indels 0; Gaps 0;

QY 1 MKHLWFFLLVAPRWVLSQVQLQDQAGLLKPKSETLSITCAVYGGSGFYWSWIRPP 60
 DB 1 MKHLWFFLLVAPRWVLSQVQLQDQAGLLKPKSETLSITCAVYGGSGFYWSWIRPP 60

QY 61 GKLEWIGELNHSSTNYPNLSKRVITISVDTSKNOFSLKLSVTADTAAYVCAR 116
 DB 61 GKLEWIGELNHSSTNYPNLSKRVITISVDTSKNOFSLKLSVTADTAAYVCAR 116

RESULT 9
 ID W01822 standard; Protein: 476 AA.
 AC W01822;
 DT 25-MAY-1997 (first entry)
 DE Primatised anti-human B7.1 antigen antibody 16C10 heavy chain.
 KW Monoclonal antibody; cynomolgus monkey; macaque; 16C10;
 KW primatised antibody; B7 antigen; CD28; Immunosuppressive;
 KW autoimmune disease; idiopathic thrombocytopenia purpura;
 KW systemic lupus erythematosus; rheumatoid arthritis; psoriasis;
 KW type 1 diabetes mellitus; graft versus host disease;
 KW hetero-hybridoma; transfectoma.
 OS Chimeric Macaca cynomolgus;
 OS Chimeric Homo sapiens.
 PN WO9640878-A1.
 PD 19-DEC-1996.
 PF 06-JUN-1996; U10053.
 PR 07-JUN-1995; US-487550.
 PA (IDEC-) IDEC PHARM CORP.
 PA Anderson DR, Brans P, Hanna N, Shestowsky WS;
 PI WPI: 97-108638/10.
 DR N-PSDB; T62513.
 PT Monkey monoclonal antibody binding human B7.1 or B7.2 antigen -
 PT useful for treating autoimmune disease or graft-versus-host disease
 PS Claim 14; Fig 10B; 81pp; English.
 CC 2 Polypeptides (W01821 and W01822) respectively comprise primatised
 CC forms of the light and heavy chains of cynomolgus monkey anti-human
 CC B7.1 antigen monoclonal antibody 16C10. Cloned 16C10 light and
 CC heavy variable genes (see also T62512 and T62513) are inserted into
 CC an expression vector (pref. NEOSPR4) which contains human light and
 CC heavy chain constant region genes to allow prodn. of the primatised
 CC antibody in e.g. CHO cells. Primatised 7C10 and 7B6 anti-B7.1
 CC antibodies have also been produced (see also W01817-20). The
 CC primatised antibodies inhibit the B7:CD28 pathway, making them
 CC useful immunosuppressants for the treatment of autoimmune disorders
 CC and graft-versus-host disease.
 SQ Sequence 476 AA;

Query Match 72.4%; Score 541.5; DB 1; Length 476;
 Best Local Similarity 74.0%; Pred. No. 7.7e-38;
 Matches 108; Conservative 11; Mismatches 20; Indels 7; Gaps 3;

QY 1 MKHLWFFLLVAPRWVLSQVQLQDQAGLLKPKSETLSITCAVYGGSGFYWSWIRPP 59
 DB 1 MKHLWFFLLVAPRWVLSQVQLQDQAGLLKPKSETLSITCAVYGGSGFYWSWIRPP 60

PT produced by primer amplification, used in the diagnosis of HCMV
 PT Infection
 PS Claim 4: Page 16-18: 22pp; Japanese.
 CC The sequences given in R6553-54 represent the heavy and light chains
 CC respectively of a monoclonal antibody against a 65 kD antigen of human
 CC cytomegalovirus (HCMV). The DNA's encoding these sequences were
 CC amplified using the sequences given in T18040-58. The monoclonal
 CC antibody may be used in the diagnosis of HCMV.
 SO Sequence 475 AA;

Query Match 72.1%; Score 539; DB 1; Length 475;
 Best Local Similarity 74.5%; Pred. No. 1.2e-37;
 Matches 111; Conservative 6; Mismatches 18; Indels 14; Gaps 3;

OY 1 MKHMFLLVAPRWLSQVLOQMGAGLKPSETSLTCAYVGGSF--SGYWSMIRQ 58
 DB 1 MKHMFLLVAPRWLSQVLOQMGAGLKPSETSLTCAYVGGSF--SGYWSMIRQ 60
 59 PGKGLMEIGINSGSTYNPSLSKRVTSVDTSKNOFSKLSTVTAADTAVYCAR 118
 DB 61 PGKGLMEIGITGSGSTYNPSLSKRVTSVDSNNQFSLKSTVTAADTAVYCAR-- 118
 OY 119 AARPHRYD-----YMGGLTVTVSS 139
 DB 119 -TSQYDILTGSPSYWGGLTVTVSS 145

RESULT 13
 ID R66298 standard; Protein; 116 AA.
 AC R66298;
 DT 07-AUG-1995 (first entry)
 DE Human immunoglobulin variable heavy chain #4.
 KW Primer; PCR; amplify; human; immunoglobulin; variable; heavy chain;
 KW cosmid; placenta; vector; pJB81; E.coli; mammalian.
 OS Homo sapiens.
 PN M09426895-A.
 PD 24-NOV-1994.
 PF 10-MAY-1993; J00603.
 PR 10-MAY-1993; NO-J00603.
 PA (NIBS) JAPAN TOBACCO INC.
 PI Honjo T, Matsuda F;
 DR N-PSDB; 078942.
 PT DNA fragment comprising human immunoglobulin Vh genes - for the
 PT production of human immunoglobulin in mammalian hosts
 P1 disclosure: Page 34-35; 130pp; Japanese.
 CC Protein sequences (R66295-51) are novel human immunoglobulin heavy chain
 CC sequences encoded by novel isolated genes. The genes (078939-79002) were
 CC isolated and cloned from a series of cosmid constructs: Y202; Y103; Y21;
 CC Y6; Y4; 3-31; M84; M18 and M31, by PCR amplification using primers
 CC 078917-38. The genes are subdivided into 5 families of Vh genes. The
 CC fragments cover a region of 800 kb. The DNA fragments were isolated from
 CC high molecular weight DNA from human placenta. The DNA was partially
 CC digested with Taqi restriction enzyme. The fragments were separated by
 CC gel electrophoresis and 35-45 kb fractions were collected. The fragments
 CC products were ligated with ClaI-digested cosmid vector pJB81. The ligation
 CC fragments were then subcloned and infected into E.coli 490A. The
 CC the DNA fragments encoding them are useful in producing human
 CC immunoglobulin in mammalian hosts.
 SO Sequence 116 AA;

Query Match 71.9%; Score 538; DB 1; Length 116;
 Best Local Similarity 88.8%; Pred. No. 3.5e-38;
 Matches 103; Conservative 3; Mismatches 10; Indels 0; Gaps 0;
 OY 1 MKHMFLLVAPRWLSQVLOQMGAGLKPSETSLTCAYVGGSFSGSYWSMIRP 60
 DB 1 MKHMFLLVAPRWLSQVLOQMGAGLKPSETSLTCAYVGGSFSGSYWSMIRP 60

OY 61 GKGLMEIGINSGSTYNPSLSKRVTSVDTSKNOFSKLSTVTAADTAVYCAR 116
 DB 61 GKGLMEIGITGSGSTYNPSLSKRVTSVDSNNQFSLKSTVTAADTAVYCAR 116

RESULT 14
 ID W32477 standard; Protein; 140 AA.
 AC W32477;
 DT 16-JAN-1998 (first entry)
 DE Anti-CD4 cynomolgus monkey immunoglobulin heavy chain variable region.
 KW Anti-CD4 antibody; cynomolgus monkey; immunoglobulin; Ig;
 KW chimpanzee; chimeric antibody; human therapy; Old World monkey;
 KW antigen binding region; tumour.
 OS Macaca fascicularis.
 PN US5658570-A.
 PD 19-AUG-1997.
 PF 25-JUL-1991; 735064.
 PR 10-JUL-1992; US-912292.
 PR 25-JUL-1991; US-735064.
 PR 23-MAR-1992; US-856281.
 PR 25-JAN-1993; US-379072.
 PA (IDEC-) IDEC PHARM CORP.
 PI Hanna N, Newman RA, Raab RW;
 DR N-PSDB; T91564.
 PT Chimeric antibodies for human therapy - comprising human or
 PT chimpanzee immunoglobulin constant region and an Old World monkey
 PT antigen-binding region
 PS Example 3; Fig 13; 46pp; English.
 CC A new chimeric antibody (Ab) has been developed comprising a human or
 CC chimpanzee immunoglobulin (Ig) constant region and an Old World monkey
 CC antigen (Ag)-binding region. The present sequence represents an anti-CD4
 CC cynomolgus monkey Ig heavy chain variable region. An anti-CD4 antibody
 CC (Ab) comprising the light- and heavy-chain variable regions encoded by
 CC DNA corresponding to the present sequence, and that of T91565, is also
 CC new. The Abs are useful for human therapy, especially of tumours. Old
 CC World monkeys are sufficiently different from humans to allow Abs
 CC against human Ags, even relatively conserved Ags such as CD4 and CD54,
 CC to be raised in these monkeys, and are sufficiently similar to humans to
 CC avoid host anti-Ab immune responses when the Abs are introduced into
 CC humans.
 SO Sequence 140 AA;

Query Match 71.7%; Score 536.5; DB 1; Length 140;
 Best Local Similarity 77.3%; Pred. No. 5.7e-38;
 Matches 109; Conservative 7; Mismatches 22; Indels 3; Gaps 3;

OY 1 MKHMFLLVAPRWLSQVLOQMGAGLKPSETSLTCAYVGGSFSGSYWSMIRP 59
 DB 1 MKHMFLLVAPRWLSQVLOQMGAGLKPSETSLTCAYVGGSFSGSYWSMIRP 60
 OY 60 PGKGLMEIGINSGSTYNPSLSKRVTSVDTSKNOFSKLSTVTAADTAVYCAR 118
 DB 61 PGKGLMEIGITGSGSTYNPSLSKRVTSVDSNNQFSLKSTVTAADTAVYCAR 120
 OY 119 AARPHRYD-----YMGGLTVTVSS 139
 DB 121 LKYLH-WLLYMGGLTVTVSS 140

RESULT 15
 ID W43430 standard; Protein; 140 AA.
 AC W43430;
 DT 05-MAY-1998 (first entry)
 DE Monkey anti-CD4 heavy chain variable region protein sequence.
 KW Primer; PCR; amplification; leader sequence; human; monkey; baboon;
 KW macaque; immunoglobulin; heavy chain variable region; chimpanzee; hybrid;
 KW lymphoma; AIDS; autoimmune disease; inflammatory disease; transplant;
 KW tumour; antibody.
 OS Macaca cynomolgus.

FH Key Location/Qualifiers
 FT Peptide 1..19 /note="signal peptide"
 FT Protein 20..140 /note="mature protein"
 FT US5693780-A.
 PN 02-DEC-1997.
 PD 07-JUN-1995; 481869.
 PR 10-JUL-1992; US-912292.
 PR 25-JUL-1991; US-735064.
 PR 23-MAR-1992; US-856281.
 PR 25-JAN-1995; US-379072.
 PR 07-JUN-1995; US-481869.
 PA (IDEC-) IDEC PHARM CORP.
 PI Hanna N, Newman RA, Raab RW;
 DR WPI: 98-031820/03.
 DR N-PSDB: V05695.
 PT Nucleic acid encoding hybrid antibody - comprising monkey
 PT antigen-binding region and human or chimp constant region
 P Example 3; Fig 13; 46pp; English.
 C This sequence represents the heavy chain variable region from an
 CC anti-human CD4 immunoglobulin raised in cynomolgus monkeys. The coding
 CC sequence was PCR amplified and used in the construction of a recombinant
 CC antibody comprising: (1) an Old World monkey Ig antigen-binding region;
 CC and (11) a human or chimpanzee Ig constant region. The hybrid antibodies
 CC can be used as passive or active therapeutic agents against human
 CC diseases, e.g. B-cell lymphoma, AIDS, autoimmune and inflammatory
 CC diseases, transplant rejection or tumours, or for producing therapeutic
 CC and diagnostic conjugates. Although evolutionary distant monkeys are
 CC used to raise antibodies against human antigens, they are sufficiently
 CC similar that they produce antibodies similar to human antibodies, such
 CC that when the monkey antibodies are introduced into humans, no host
 CC anti-antibody response is stimulated.
 SQ Sequence 140 AA;

Query Match 71.7%; Score 536.5; DB 1; Length 140;
 Best Local Similarity 77.3%; Pred. No. 5.7e-38;
 Matches 109; Conservative 7; Mismatches 22; Indels 3; Gaps 3;

QY 1 MKHLMFLLVAAPRWVLSQVQLQOGAGLKPSETLSLTCAVYGGSG-YVMSWIRQP 59
 DB 1 MKHLMFLLVAAPRWVLSQVQLQOGAGLKPSETLSLTCAVYGGSG-YVMSWIRQP 59
 QY 60 PGKGLWIGETIHS-GSTNYPNLSKRYTISVDTSKNOFSKLSVTADTAIVYCCAREI 118
 DB 61 PGKGLWIGETIHS-GSTNYPNLSKRYTISVDTSKNOFSKLSVTADTAIVYCCAREI 118
 119 AARPHRYFDYWGQGLVTVSS 139
 DB 121 LKYLH-WLLYWGQGLVTVSS 140

Search completed: July 26, 2000, 14:01:26
 Job time: 2765 sec

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GenCore version 4.5
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OM protein - protein search, using sw model

Run on: July 26, 2000, 13:24:00 ; Search time 43.23 Seconds

(without alignments)
198.982 Million cell updates/sec

Title: US-09-203-768a-2

Perfect score: 748
Sequence: 1 MKHLMFLLVAAPRWLSQ.....ARPHRFDPYWGGLTVVSS 139

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Sequences: 178050 seqs, 61884766 residues

Minimum DB seq length: 0
Maximum DB seq length: 1000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :
1: PIR:64:*
2: PIR:1:*
3: PIR:2:*
4: PIR:4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|-------|-------------|--------|----------|--------------------|
| 1 | 685.5 | 91.6 | 140 | 2 A49045 | Ig heavy chain V r |
| 2 | 641 | 85.7 | 140 | 2 S78052 | Ig heavy chain pre |
| 3 | 625.5 | 83.6 | 140 | 2 I37782 | Ig variable region |
| 4 | 589 | 78.7 | 139 | 2 S31586 | Ig heavy chain V r |
| 5 | 585 | 78.2 | 137 | 2 S31576 | Ig heavy chain V r |
| 6 | 584.5 | 78.1 | 147 | 2 S13519 | Ig heavy chain V r |
| 7 | 576 | 77.0 | 145 | 2 S78055 | Ig heavy chain pre |
| 8 | 571.5 | 76.4 | 146 | 1 G1H0H2 | Ig heavy chain pre |
| 9 | 571 | 76.3 | 126 | 2 S47010 | Ig heavy chain V4. |
| 10 | 570.5 | 76.3 | 139 | 2 S31596 | Ig heavy chain V r |
| 11 | 569.5 | 76.1 | 155 | 2 S31511 | Ig heavy chain - h |
| 12 | 563.5 | 75.3 | 155 | 2 S31512 | Ig heavy chain - h |
| 13 | 560.5 | 74.9 | 146 | 2 S09711 | Ig heavy chain V r |
| 14 | 558 | 74.6 | 231 | 2 B23746 | Ig Fab region IV-J |
| 15 | 554.5 | 74.1 | 143 | 2 B49028 | Ig heavy chain V-I |
| 16 | 550 | 73.5 | 116 | 2 B26340 | Ig heavy chain pre |
| 17 | 544.5 | 72.8 | 146 | 2 S09710 | Ig heavy chain V r |
| 18 | 539 | 72.1 | 118 | 2 A26340 | Ig heavy chain pre |
| 19 | 538 | 71.9 | 116 | 2 S18557 | Ig heavy chain V r |
| 20 | 535.5 | 71.6 | 140 | 2 A24770 | Ig heavy chain V r |
| 21 | 530.5 | 70.9 | 122 | 2 J10047 | Ig heavy chain V r |
| 22 | 530 | 70.9 | 139 | 2 A41287 | Ig heavy chain pre |
| 23 | 519 | 69.4 | 139 | 2 S26806 | Ig heavy chain V r |
| 24 | 518 | 69.3 | 97 | 2 S26808 | Ig heavy chain V r |
| 25 | 518 | 69.3 | 124 | 2 S31684 | Ig heavy chain V r |
| 26 | 514.5 | 68.8 | 114 | 2 I72867 | Ig heavy chain V r |
| 27 | 514.5 | 68.8 | 130 | 2 S78051 | Ig heavy chain V r |
| 28 | 512.5 | 68.5 | 135 | 2 S78051 | Ig heavy chain pre |
| 29 | 512 | 68.4 | 143 | 2 B41287 | Ig heavy chain pre |

| | | | | | |
|----|-------|------|-----|----------|--------------------|
| 30 | 509 | 68.0 | 97 | 2 S14474 | Ig heavy chain V r |
| 31 | 508.5 | 68.0 | 137 | 2 S31585 | Ig heavy chain V r |
| 32 | 508 | 67.9 | 97 | 2 G34964 | Ig heavy chain V-I |
| 33 | 497.5 | 66.5 | 117 | 2 E34964 | Ig heavy chain pre |
| 34 | 490 | 65.5 | 97 | 2 S26805 | Ig heavy chain V r |
| 35 | 488 | 65.2 | 135 | 2 S31604 | Ig heavy chain V r |
| 36 | 483 | 64.6 | 97 | 2 S26806 | Ig heavy chain V r |
| 37 | 483 | 64.6 | 97 | 2 JH0428 | Ig gamma chain V r |
| 38 | 475 | 63.5 | 129 | 2 S44114 | Ig heavy chain V r |
| 39 | 472 | 63.1 | 97 | 2 S26808 | Ig heavy chain V r |
| 40 | 472 | 63.1 | 130 | 2 S30534 | Ig heavy chain V r |
| 41 | 466.5 | 62.4 | 121 | 2 S44113 | Ig heavy chain V r |
| 42 | 466 | 62.3 | 118 | 2 S24443 | Ig heavy chain V r |
| 43 | 464.5 | 62.1 | 123 | 2 S30530 | Ig heavy chain V r |
| 44 | 464 | 62.0 | 120 | 2 PT0370 | Ig mu chain precu |
| 45 | 463.5 | 62.0 | 127 | 2 S19668 | Ig heavy chain V r |

ALIGNMENTS

RESULT 1
A:9045
I: heavy chain V region (anti-B cell autoantibody) - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 19-Dec-1993 #sequence_revision 18-Nov-1994 #text_change 23-Jul-1999
C:Accession: A49045
R:Grillot-Courvalin, C.; Brouet, J.C.; Piller, F.; Rassenlt, L.Z.; Labaune, S.; Silve Eur. J. Immunol. 22, 1781-1788, 1992
A:Title: An anti-B cell autoantibody from Wiskott-Aldrich syndrome which recognizes 1 A:Reference number: A49045; M0ID:92324290
A:Accession: A49045
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-140 <GR1>
A:Cross-references: GB:S39381; NID:q250899; PIDN:AA322441.1; PID:q250900
A:Note: sequence extracted from NCBI backbone (NCBIN:108088, NCBI:P.108089)
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:34-116/Domain: immunoglobulin homology <IMM>

Query Match 91.6%; Score 685.5; DB 2; Length 140;
Best Local Similarity 94.3%; Pred. NO. 8e-55;
Matches 132; Conservative 0; Mismatches 7; Indels 1; Gaps 1;
QY 1 MKHLMFLLVAAPRWLSQVOLOQMGAGLKPSETSLTCAVYGGSGYMSWIRPP 60
Db 1 MKHLMFLLVAAPRWLSQVOLOQMGAGLKPSETSLTCAVYGGSGYMSWIRPP 60
QY 61 GKGLFWGELINHGSGTNYNSLSKRVTVSYDTSKNQPSLSSVTADTVYICAR-EIA 119
Db 61 GKGLFWGELINHGSGTNYNSLSKRVTVSYDTSKNQPSLSSVTADTVYICAR-EIA 120
QY 120 ARPHRFDPYWGGLTVVSS 139
Db 121 ATIVSFDPYWGGLTVVSS 140
RESULT 2
I: heavy chain precursor V-D-J region (clone mAb 63VH) - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 19-Nov-1997 #sequence_revision 05-Dec-1997 #text_change 23-Jul-1999
C:Accession: S78052; S23717
R:Harindranath, N.
Submitted to the EMBL Data Library, August 1990
A:Reference number: S78051
A:Accession: S78052
A:Molecule type: mRNA
A:Residues: 1-140 <HAR>
A:Cross-references: EMBL:X54441; NID:q37815; PIDN:CAA38308.1; PID:q930118
R:Harindranath, N.; Goldfarb, I.S.; Ikenatsu, H.; Burastero, S.E.; Wilder, R.L.; Nock

Int. Immunol. 3, 865-875, 1991
A:Title: Complete sequence of the genes encoding the V(H) and V(L) regions of low- and high-affinity B cell antigen receptors.
A:Reference number: S23716; MUID:92031262
A:Accession: S23717

A:Molecule type: mRNA
A:Residues: 15-111 <HMM>
A:Cross-references: EMBL:X54441
C:Superfamily: Immunoglobulin V region: Immunoglobulin homology
C:Keywords: Immunoglobulin
F:1-14/Domain: signal sequence (fragment) #status predicted <SIG>
F:15-140/Product: Ig heavy chain (fragment) #status predicted <MAT>
F:29-111/Domain: Immunoglobulin homology <IMM>

Query Match 85.7%; Score 641; DB 2; Length 140;
Best Local Similarity 88.7%; Pred. No. 7.9e-51;
Matches 126; Conservative 1; Mismatches 5; Indels 10; Gaps 2;

6 FELLVAAPRWLSQVQLQDQMGAGLLKPSSETLSLTCAYVGGSGFYWSWIRPPGKLE 65
1 FELLVAAPRWLSQVQLQDQMGAGLLKPSSETLSLTCAYVGGSGFYWSWIRPPGKLE 60
66 WIGELINHSSTNPNPSLKSRYTISVDTSKNPSLKLSTVTAADTAAYTCAR-----E 117
61 WIGELINHSSTNPNPSLKSRYTISVDTSKNPSLKLSTVTAADTAAYTCARSGSLG 120
118 IAPRHREFDYWGQGLTVYSS 139
121 WLLP--AFDYWGQGLTVYSS 140

RESULT 3
137782
Ig variable region (VDJ) (clone T23-9) - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 16-Feb-1996 #sequence_revision 13-Mar-1997 #text_change 23-Jul-1999
C:Accession: 137782; S25476
R:Demaison, C.; Chastagner, P.; Theze, J.; Zouali, M.
Proc. Natl. Acad. Sci. U.S.A. 91, 514-518, 1994
A:Title: Somatic diversification in the heavy chain variable region genes expressed by B cells.
A:Reference number: A36876; MUID:94119917
A:Accession: 137782
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-140 <RES>
A:Cross-references: EMBL:X67906; NID:933582; PDB:CAA8104.1; PID:933583
C:Superfamily: Immunoglobulin V region: Immunoglobulin homology
F:28/Domain: Immunoglobulin homology <IMM>

Query Match 83.6%; Score 625.5; DB 2; Length 140;
Best Local Similarity 86.4%; Pred. No. 2e-49;
Matches 121; Conservative 6; Mismatches 12; Indels 1; Gaps 1;

1 MKHLMFLLVAAPRWLSQVQLQDQMGAGLLKPSSETLSLTCAYVGGSGFYWSWIRPP 60
1 MKHLMFLLVAAPRWLSQVQLQDQMGAGLLKPSSETLSLTCAYVGGSGFYWSWIRPP 60
61 GKGLEWIGRITTSSTNPNPSLKSRYTISVDTSKNPSLKLSTVTAADTAAYTCAREIAA 120
61 GKGLEWIGRITTSSTNPNPSLKSRYTISVDTSKNPSLKLSTVTAADTAAYTCAREIAA 120
61 GKGLEWIGRITTSSTNPNPSLKSRYTISVDTSKNPSLKLSTVTAADTAAYTCAREIAA 120
121 RPH-RYFDYWGQGLTVYSS 139
121 SWYGRYFDYWGQGLTVYSS 140

RESULT 4
S31586
Ig heavy chain V region - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999

C:Accession: S31586
R:Christler, A.M.; Gauthier, L.; Boudil, L.; Fougereau, M.; Tonnelle, C.
Submitted to the EMBL Data Library, June 1992
A:Description: Mechanisms that generate human immunoglobulin diversity operate from t

A:Reference number: S31585
A:Accession: S31586
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-139 <CUT>
A:Cross-references: EMBL:Z14182; NID:930978; PDB:CAA78551.1; PID:930979
C:Superfamily: Immunoglobulin V region: Immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:34-116/Domain: Immunoglobulin homology <IMM>

Query Match 78.7%; Score 589; DB 2; Length 139;
Best Local Similarity 82.7%; Pred. No. 3.7e-46;
Matches 115; Conservative 4; Mismatches 20; Indels 0; Gaps 0;

1 MKHLMFLLVAAPRWLSQVQLQDQMGAGLLKPSSETLSLTCAYVGGSGFYWSWIRPP 60
1 MKHLMFLLVAAPRWLSQVQLQDQMGAGLLKPSSETLSLTCAYVGGSGFYWSWIRPP 60
61 GKGLEWIGRITTSSTNPNPSLKSRYTISVDTSKNPSLKLSTVTAADTAAYTCAREIAA 120
61 GKGLEWIGRITTSSTNPNPSLKSRYTISVDTSKNPSLKLSTVTAADTAAYTCAREIAA 120
121 RPHRYFDYWGQGLTVYSS 139
121 IRRGAFDYMGGQGLTVYSS 139

RESULT 5
S31676
Ig heavy chain V region - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999
C:Accession: S31676
R:Christler, A.M.; Gauthier, L.; Boudil, L.; Fougereau, M.; Tonnelle, C.
Submitted to the EMBL Data Library, June 1992
A:Description: Mechanisms that generate human immunoglobulin diversity operate from t
A:Reference number: S31676
A:Accession: S31676
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-137 <CUT>
A:Cross-references: EMBL:Z14182; NID:931031; PDB:CAA78551.1; PID:931032
C:Superfamily: Immunoglobulin V region: Immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:34-116/Domain: Immunoglobulin homology <IMM>

Query Match 78.2%; Score 585; DB 2; Length 137;
Best Local Similarity 82.9%; Pred. No. 8.3e-46;
Matches 116; Conservative 4; Mismatches 16; Indels 4; Gaps 2;

1 MKHLMFLLVAAPRWLSQVQLQDQMGAGLLKPSSETLSLTCAYVGGSGFYWSWIRPP 60
1 MKHLMFLLVAAPRWLSQVQLQDQMGAGLLKPSSETLSLTCAYVGGSGFYWSWIRPP 60
61 GKGLEWIGRITTSSTNPNPSLKSRYTISVDTSKNPSLKLSTVTAADTAAYTCAREIAA 120
61 GKGLEWIGRITTSSTNPNPSLKSRYTISVDTSKNPSLKLSTVTAADTAAYTCAREIAA 120
61 GKGLEWIGRITTSSTNPNPSLKSRYTISVDTSKNPSLKLSTVTAADTAAYTCAREIAA 120
121 RPHRYFDYWGQGLTVYSS 139
118 APLMYGMDYWGQGLTVYSS 137

RESULT 6
S13519
Ig heavy chain V region precursor - human
C:Species: Homo sapiens (man)

C>Date: 25-Feb-1994 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999
C/Accession: S13519
R:Mortari, F.; Ochis, H.D.; Wedgwood, R.J.P.; Schroeder Jr., H.M.
Nucleic Acids Res. 19, 673, 1991
A/Title: Immunoglobulin variable heavy chain cDNA sequence from a patient with X-linked
A/Reference number: S13519; MUID:9118791
A/Accession: S13519
A/Status: preliminary
A/Molecule type: mRNA
A/Residues: 1-147 <MOR>
A/Cross-references: EMBL:X56158; NID:q37724; PIDN:CAA3626.1; PID:q37725
C/Superfamily: Immunoglobulin V region; Immunoglobulin homology
C/Keywords: heterotetramer; Immunoglobulin
F:41-125/Domain: Immunoglobulin homology <IM>

Query Match 78.1%; Score 584.5; DB 2; Length 147;
Best Local Similarity 82.3%; Pred. No. 9.9e-46;
Matches 116; Conservative 5; Mismatches 17; Indels 3; Gaps 2;

1 MKHMFLLVAAPRWVLSQVQLQWAGLSPKSELTSLCAVYGGSF--SGYYSWIRQ 58
|||||
8 MKHMFLLVAAPRWVLSQVQLQWAGLSPKSELTSLCAVYGGSFSSSSSYWGIRO 67

59 PPGKLEWIGELNHSGSTNYPNLSKSRVTISVDTSKNOFSLKLSVTADTAVYVCAREI 118
|||||
68 PPGKLEWIGELNHSGSTNYPNLSKSRVTISVDTSKNOFSLKLSVTADTAVYVCARPL 127

119 AARPRYEDYWGQGLTVTVSS 139
|||||
128 LMF-GELEDYWGQGLTVTVSS 147

RESULT 7
578055 Ig heavy chain precursor V-D-J region (clone mAb 67VH) - human (fragment)

C/Species: Homo sapiens (man)
C/Date: 19-Nov-1997 #sequence_revision 05-Dec-1997 #text_change 23-Jul-1999
C/Accession: S78055; S23720
R:Haridranath, N.
Submitted to the EMBL Data Library, August 1990

A/Reference number: S78051

A/Accession: S78055
A/Molecule type: mRNA

A/Residues: 1-145 <HAR>

A/Cross-references: EMBL:X54445; NID:q37817; PIDN:CAA36312.1; PID:q37818

R:Haridranath, N.; Goldfarb, I.S.; Ikematsu, H.; Burastero, S.E.; Wilder, R.L.; Notkins
Immunol. 3, 865-875, 1991

Complete sequence of the gene encoding the V(H) and V(L) regions of low- and h
patient.

A/Reference number: S23716; MUID:92031262

A/Accession: S23720

A/Molecule type: mRNA

A/Residues: 18-115 <HAW>

A/Cross-references: EMBL:X54445

A/Note: the authors translated the codon GCA for residue 67 as Arg

C/Superfamily: Immunoglobulin V region; Immunoglobulin homology

C/Keywords: Immunoglobulin

F:1-17/Domain: signal sequence (fragment) #status predicted <SIG>
F:18-145/Product: Ig heavy chain (fragment) #status predicted <MAT>
F:32-115/Domain: Immunoglobulin homology <IM>

Query Match 77.0%; Score 576; DB 2; Length 145;
Best Local Similarity 79.5%; Pred. No. 5.7e-45;
Matches 116; Conservative 6; Mismatches 14; Indels 10; Gaps 3;

3 HUMFLLVAAPRWVLSQVQLQWAGLSPKSELTSLCAVYGGSF--SGYYSWIRQPPG 61
|||||

1 HUMFLLVAAPRWVLSQVQLQWAGLSPKSELTSLCAVYGGSFSSSSSYWGIROPPG 60
|||||

62 KGLEWIGELNHSGSTNYPNLSKSRVTISVDTSKNOFSLKLSVTADTAVYVCAREIA- 120
|||||

Db 61 KGLEWIGELNHSGSTNYPNLSKSRVTISVDTSKNOFSLKLSVTADTAVYVCAREI 120

121 -----RPRHYEDYWGQGLTVTVSS 139
|||||

121 FWSGYTRGY-YFDYWGQGLTVTVSS 145
|||||

RESULT 8

61HWH2

Ig heavy chain precursor V-II region (ARH-77) - human

C/Species: Homo sapiens (man)

C/Date: 30-Jun-1987 #sequence_revision 30-Jun-1987 #text_change 02-Sep-1997

C/Accession: A02101

R:Kudo, A.; Ishihara, T.; Nishimura, Y.; Watanabe, T.
Gene 33, 181-189, 1985

A/Title: A cloned human immunoglobulin heavy chain gene with a novel direct-repeat se

A/Reference number: A02101; MUID:85205332

A/Accession: A02101

A/Molecule type: mRNA

A/Residues: 1-146 <KUD>

A/Note: the sequence was determined from the differentiated gene

A/Note: the authors translated the codon GGG for residue 17 as Arg

C/Genetics:

A/Gene: GDB:IGHV

A/Cross-references: GDB:128528; OMIM:147070

A/Map position: 14q32.33-14q32.33

A/Introns: 16/3

C/Superfamily: Immunoglobulin V region; Immunoglobulin homology

C/Keywords: heterotetramer; Immunoglobulin

F:1-19/Domain: signal sequence #status predicted <SIG>

F:20-146/Product: Ig heavy chain V-II region (ARH-77) #status predicted <MAT>

F:20-117/Region: V segment

F:35-117/Domain: Immunoglobulin homology <IM>

F:118-127/Region: D segment

F:128-146/Region: J segment

F:42-115/Disulfide bonds: #status predicted

Query Match 76.4%; Score 571.5; DB 1; Length 146;
Best Local Similarity 78.1%; Pred. No. 1.5e-44;
Matches 114; Conservative 5; Mismatches 20; Indels 7; Gaps 2;

1 MKHMFLLVAAPRWVLSQVQLQWAGLSPKSELTSLCAVYGGSFSGYYSWIRQ 59
|||||

1 MKHMFLLVWCQLPDVGLSQVQLQWAGLSPKSELTSLCAVYGGSFSGYYSWIRQ 60
|||||

60 PPGKLEWIGELNHSGSTNYPNLSKSRVTISVDTSKNOFSLKLSVTADTAVYVCAREIA 119
|||||

61 PPGKLEWIGELNHSGSTNYPNLSKSRVTISVDTSKNOFSLKLSVTADTAVYVCAREIA 120
|||||

120 AARPRYEDY-----WGQGLTVTVSS 139
|||||

121 RGNWVDVYGGMDYWGQGLTVTVSS 146
|||||

RESULT 9

S47010 Ig heavy chain V4.21-Uniqued-J5 region - human

C/Species: Homo sapiens (man)

C/Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 23-Jul-1999

C/Accession: S47010

R:Mahmoudi, M.; Gasyna, E.; Denomme, G.; Edwards, J.; Bell, D.; Cairns, E.
submitted to the EMBL Data Library, July 1994

A/Description: The role of the immunoglobulin heavy chain in human anti-DNA antibody

A/Reference number: S47009

A/Accession: S47010

A/Status: preliminary

A/Molecule type: mRNA

A/Residues: 1-126 <MAH>

A/Cross-references: EMBL:Z35492; NID:q517254; PIDN:CAA84625.1; PID:q517255

C/Superfamily: Immunoglobulin V region; Immunoglobulin homology

C/Keywords: heterotetramer; Immunoglobulin
F:15-97/Domain: Immunoglobulin homology <IM>

Query Match 76.3%; Score 571; DB 2; Length 126;
Best Local Similarity 87.3%; Pred. No. 1.4e-44;

Matches 110; Conservative 3; Mismatches 7; Indels 6; Gaps 1;

OY 20 QVQLQMGAGLLKPSSETLSITCAVYGGSFSGYWSWIROPKGLMGEINHSSTNN 79

DB 1 QVQLQMGAGLLKPSSETLSITCAVYGGSFSGYWSWIROPKGLMGEINHSSTNN 60

OY 80 PSIKSVTISVDSKNOFSLKSVTAADTAVYCAR-----ETARRHRYFDYGGGT 133

DB 61 PSIKSVTISVDSKNOFSLKSVTAADTAVYCARGGCCPKKASCYTKNFDPMWGGGT 120

OY 134 LVTYSS 139

DB 121 LVTYSS 126

RESULT 10
S31512

Ig heavy chain V region - human (fragment)

C:Species: Homo sapiens (man)

C>Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999

C:Accession: S31512

R:Chastagner, A.M.; Gauthier, L.; Boubil, L.; Fougereau, M.; Tonnelie, C.

submitted to the EMBL Data Library, June 1992

A:Description: Mechanisms that generate human immunoglobulin diversity operate from the

A:Reference number: S31585

A:Accession: S31586

A>Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-139 <CD>

A:Cross-references: EMBL:Z14194; NID:930975; PIDN:CAA78563.1; PID:930976

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

F:34-116/Domain: immunoglobulin homology <IMM>

Query Match 76.3%; Score 570.5; DB 2; Length 139;
Best Local Similarity 81.5%; Pred. No. 1.7e-44;

Matches 110; Conservative 6; Mismatches 18; Indels 1; Gaps 1;

OY 1 MKHMFLLVAAPRWVLSQVQLQMGAGLLKPSSETLSITCAVYGGSFSGYWSWIROP 60

DB 1 MKHMFLLVAAPRWVLSQVQLQMGAGLLKPSSETLSITCAVYGGSFSGYWSWIROP 60

OY 61 GKGLMGEINHSSTNNPSLKSRTISVDSKNOFSLKSVTAADTAVYCAR-EIA 119

DB 61 AKGLEWIGRITTSSTNNPSLKSRTISVDSKNOFSLKSVTAADTAVYCARGGIG 120

OY 120 ARPHRYFDYGGGT 134

DB 121 LTGDKMIDYWGGL 135

RESULT 11
S31511

Ig heavy chain - human

C:Species: Homo sapiens (man)

C>Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 23-Jul-1999

C:Accession: S31511

R:Chastagner, P.; Demaison, C.; Theze, J.; Zouali, M.

submitted to the EMBL Data Library, December 1992

A:Description: Dominance of clonotypic patterns and variable gene usage of anti-DNA auto

A:Reference number: S31509

A:Accession: S31511

A>Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-155 <CH>

A:Cross-references: EMBL:X69866; NID:933094; PIDN:CAA49500.1; PID:933095

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

F:47-129/Domain: immunoglobulin homology <IMM>

Query Match 76.1%; Score 569.5; DB 2; Length 155;
Best Local Similarity 77.8%; Pred. No. 2.3e-44;

Matches 112; Conservative 7; Mismatches 18; Indels 7; Gaps 2;

OY 1 MKHMFLLVAAPRWVLSQVQLQMGAGLLKPSSETLSITCAVYGGSFSGYWSWIROP 60

DB 14 MKHMFLLVAAPRWVLSQVQLQMGAGLLKPSSETLSITCAVYGGSFSGYWSWIROP 73

OY 61 GKGLMGEINHSSTNNPSLKSRTISVDSKNOFSLKSVTAADTAVYCAR-ETAA 120

DB 74 GKGLMGEINHSSTNNPSLKSRTISVDSKNOFSLKSVTAADTAVYCAR--GG 131

OY 121 RPHRYDY----WGGLTYVSS 139

DB 132 GISSWYDYGMWGGGT 155

RESULT 12
S31512

Ig heavy chain - human

C:Species: Homo sapiens (man)

C>Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 23-Jul-1999

C:Accession: S31512

R:Chastagner, P.; Demaison, C.; Theze, J.; Zouali, M.

submitted to the EMBL Data Library, December 1992

A:Description: Dominance of clonotypic patterns and variable gene usage of anti-DNA a

A:Reference number: S31509

A:Accession: S31512

A>Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-155 <CH>

A:Cross-references: EMBL:X69860; NID:933082; PIDN:CAA49494.1; PID:933083

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

F:47-129/Domain: immunoglobulin homology <IMM>

Query Match 75.3%; Score 563.5; DB 2; Length 155;
Best Local Similarity 78.9%; Pred. No. 8.1e-44;

Matches 112; Conservative 8; Mismatches 19; Indels 3; Gaps 2;

OY 1 MKHMFLLVAAPRWVLSQVQLQMGAGLLKPSSETLSITCAVYGGSFSGYWSWIROP 60

DB 14 MKHMFLLVAAPRWVLSQVQLQMGAGLLKPSSETLSITCAVYGGSFSGYWSWIROP 73

OY 61 GKGLMGEINHSSTNNPSLKSRTISVDSKNOFSLKSVTAADTAVYCAR--ET 118

DB 74 GKGLMGEINHSSTNNPSLKSRTISVDSKNOFSLKSVTAADTAVYCARGGIG 133

OY 119 ARPHRY-FDYWGGLTYVSS 139

DB 134 SSWYVYDYGMWGGGT 155

RESULT 13
S09711

Ig heavy chain V region - human

C:Species: Homo sapiens (man)

C>Date: 21-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 16-Aug-1996

C:Accession: S09711

R:Bughes-Jones, N.C.; Bye, J.M.; Beale, D.; Coadwell, J.

Biochem. J. 268: 135-140, 1990

A:Title: Nucleotide sequences and three-dimensional modelling of the VH and VL domain

A:Reference number: S09710; MUID:9026235

A:Accession: S09711

A>Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-146 <HD>

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

Wed Jul 26 15:40:43 2000

us-09-208-768a-2.rpr

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: July 26, 2000, 14:03:14 ; Search time 12.18 Seconds

(without alignments)
353.652 Million cell updates/sec

Title: US-09-203-768a-2
Perfect score: 748

Sequence: 1 MKHLMEFLLVAPRWLSQ.....ARPHRYDYGCGTLVTSS 139

Scoring table: BIOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 85661 seqs, 30989116 residues

To: number of hits satisfying chosen parameters: 85661

Minimum DB seq length: 0
Maximum DB seq length: 1000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_38:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description |
|------------|-------|-------------|--------|----|--------------------|
| 1 | 571.5 | 76.4 | 146 | 1 | P06331 homo sapien |
| 2 | 411.5 | 55.0 | 129 | 1 | P01824 homo sapien |
| 3 | 408 | 54.5 | 137 | 1 | P01822 mus musculu |
| 4 | 397.5 | 53.1 | 117 | 1 | P01825 homo sapien |
| 5 | 370 | 49.5 | 116 | 1 | P01831 mus musculu |
| 6 | 369.5 | 49.4 | 144 | 1 | P01819 mus musculu |
| 7 | 359.5 | 48.1 | 113 | 1 | P01823 mus musculu |
| 8 | 359.5 | 48.1 | 135 | 1 | P20957 xenopus lae |
| 9 | 343 | 45.9 | 116 | 1 | P01832 mus musculu |
| 10 | 330 | 44.1 | 139 | 1 | P01751 mus musculu |
| 11 | 329 | 44.0 | 137 | 1 | P01755 mus musculu |
| 12 | 328 | 43.9 | 119 | 1 | P01807 mus musculu |
| 13 | 326.5 | 43.6 | 117 | 1 | P01853 mus musculu |
| 14 | 326 | 43.6 | 119 | 1 | P01808 mus musculu |
| 15 | 325 | 43.4 | 119 | 1 | P01810 mus musculu |
| 16 | 323.5 | 43.2 | 138 | 1 | P03980 mus musculu |
| 17 | 322 | 43.0 | 122 | 1 | P01768 homo sapien |
| 18 | 321 | 42.9 | 136 | 1 | P20956 xenopus lae |
| 19 | 317.5 | 42.4 | 117 | 1 | P01811 mus musculu |
| 20 | 316.5 | 42.3 | 118 | 1 | P01809 mus musculu |
| 21 | 316.5 | 42.3 | 142 | 1 | P01805 rattus norv |
| 22 | 316 | 42.2 | 115 | 1 | P01820 mus musculu |
| 23 | 310 | 41.4 | 120 | 1 | P03929 mus musculu |
| 24 | 308.5 | 41.0 | 123 | 1 | P01791 mus musculu |
| 25 | 305.5 | 40.8 | 121 | 1 | P01791 mus musculu |
| 26 | 304 | 40.6 | 116 | 1 | P01821 mus musculu |
| 27 | 303.5 | 40.6 | 115 | 1 | P01765 homo sapien |
| 28 | 303.5 | 40.6 | 117 | 1 | P01812 mus musculu |
| 29 | 302.5 | 40.4 | 117 | 1 | P01757 mus musculu |
| 30 | 302.5 | 40.4 | 140 | 1 | P01746 mus musculu |
| 31 | 300.5 | 40.2 | 117 | 1 | P01756 mus musculu |
| 32 | 300.5 | 40.2 | 121 | 1 | P01771 homo sapien |
| 33 | 299 | 40.0 | 147 | 1 | P04438 homo sapien |

| | | | | | | |
|----|-------|------|-----|---|------------|--------------------|
| 34 | 297 | 39.7 | 120 | 1 | HY2B_HUMAN | P01815 homo sapien |
| 35 | 296 | 39.6 | 118 | 1 | HY51_MOUSE | P06330 mus musculu |
| 36 | 295.5 | 39.5 | 120 | 1 | HY03_MOUSE | P01747 mus musculu |
| 37 | 295.5 | 39.5 | 123 | 1 | HY18_MOUSE | P01787 mus musculu |
| 38 | 295.5 | 39.5 | 123 | 1 | HY19_MOUSE | P01788 mus musculu |
| 39 | 294.5 | 39.4 | 123 | 1 | HY23_MOUSE | P01792 mus musculu |
| 40 | 293 | 39.2 | 122 | 1 | HY3H_HUMAN | P01769 homo sapien |
| 41 | 292.5 | 39.1 | 119 | 1 | HY2C_HUMAN | P01816 homo sapien |
| 42 | 290.5 | 38.8 | 117 | 1 | HY04_MOUSE | P01748 mus musculu |
| 43 | 289.5 | 38.6 | 117 | 1 | HY17_MOUSE | P01786 mus musculu |
| 44 | 288 | 38.5 | 122 | 1 | HY20_MOUSE | P01789 mus musculu |
| 45 | 287.5 | 38.4 | 116 | 1 | HY36_MOUSE | P01806 mus musculu |

ALIGNMENTS

| RESULT | ID | HY2I_HUMAN | STANDARD: | PRT: | 146 AA. |
|---|--|---|-----------|---------|------------------------------------|
| AC | P06331 | | | | |
| DT | 01-JAN-1988 (Rel. 06, Created) | | | | |
| DT | 01-JAN-1988 (Rel. 06, Last sequence update) | | | | |
| DT | 15-JUL-1999 (Rel. 38, Last annotation update) | | | | |
| DE | IG HEAVY CHAIN V-II REGION ARH-77 PRECURSOR. | | | | |
| OS | Homo sapiens (Human). | | | | |
| OC | Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; | | | | |
| OC | Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo. | | | | |
| RN | [1] | | | | |
| RP | SEQUENCE FROM N.A. | | | | |
| RX | MEDLINE: 85205332. | | | | |
| RA | Kudo A., Ishihara T., Nishimura Y., Watanabe T.; | | | | |
| RT | "A cloned human immunoglobulin heavy chain gene with a novel direct- | | | | |
| RL | repeat sequence in 5' flanking region." | | | | |
| DR | Gene 33:181-189(1985). | | | | |
| DR | PIR: A02101; G1HGH2. | | | | |
| DR | HSSP: P01825; 7FAB. | | | | |
| DR | PFAM: PF00047; 4g; 1. | | | | |
| KW | Immunoglobulin V region; Signal. | | | | |
| FT | SIGNAL | 1 | 19 | | |
| FT | CHAIN | 20 | 146 | | IG HEAVY CHAIN V-II REGION ARH-77. |
| FT | DOMAIN | 20 | 117 | | V SEGMENT. |
| FT | DOMAIN | 118 | 127 | | D SEGMENT. |
| FT | DOMAIN | 128 | 146 | | J SEGMENT. |
| FT | DISULFID | 42 | 115 | | BY SIMILARITY. |
| FT | NON_TER | 146 | 146 | | |
| SQ | SEQUENCE | 146 AA; 16228 MW; 807FDS2B218171F CRC64; | | | |
| Query Match | | | | | |
| Best Local Similarity 76.4%; Score 571.5; DB 1; Length 146; | | | | | |
| Matches 114; Conservative 5; Mismatches 20; Indels 7; Gaps 2; | | | | | |
| QY | 1 | MKHLMEFLLVAPRWLSQVQLQDGMGGLKPKSETISLTCAVYGGSGSYGWSINRP 59 | | | |
| DB | 1 | MKHLMEFLLVAPRWLSQVQLQDGMGGLKPKSETISLTCAVYGGSGSYGWSINRP 60 | | | |
| QY | 60 | PKGLEWIGEINHSSTNPNPSIKSRVTISVDTSKNQFSLKSTYADTAVYICAREIA 119 | | | |
| DB | 61 | PKGLEWIGEINHSSTNPNPSIKSRVTISVDTSKNQFSLKSTYADTAVYICAREIA 120 | | | |
| QY | 120 | ARPHRYFDY-----WGQGLTVTSS 139 | | | |
| DB | 121 | RGQWMDVYVYGGMDVWGQGLTVTSS 146 | | | |
| RESULT 2 | | | | | |
| ID | HY2F_HUMAN | STANDARD: | PRT: | 129 AA. | |
| AC | P01824 | | | | |
| DT | 21-JUL-1986 (Rel. 01, Created) | | | | |
| DT | 21-JUL-1986 (Rel. 01, Last sequence update) | | | | |
| DT | 15-JUL-1999 (Rel. 38, Last annotation update) | | | | |

DE IG HEAVY CHAIN V-II REGION WASH.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 RN Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 RP [1]
 RX MEDLINE; 82222235.
 RA Takahashi N., Tetaert D., Debaille B., Lin L.-C., Putnam F.W.;
 RT "Complete amino acid sequence of the delta heavy chain of human
 immunoglobulin D.";
 RL Proc. Natl. Acad. Sci. U.S.A. 79:2850-2854(1982).
 CC -1- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM AN IGD MYELOMA
 CC PROTEIN.
 DR PIR; A02099; D2HUMA.
 DR HSSP; P01825; 7FAB.
 DR PFAM; PF00047; 1g; 1.
 KW Immunoglobulin V region.
 FT NON_TER 129 129
 SE SEQUENCE 129 AA; 14117 MW; D5D3D47ABE51319 CRC64;

Query Match 55.0%; Score 411.5; DB 1; Length 129;
 Best Local Similarity 62.1%; Pred. No. 8.4e-33;
 Matches 82; Conservative 14; Mismatches 21; Indels 15; Gaps 3;

QY 20 QVQLQDAGAGLLKPSSETLTCAVYGGSF--SGYWSWIRPPGKLEWIGENHSGSTN 77
 Db 1 RLGQESGPGLVKPSSELTSLCIYSGGIRRTGYWGMIRPPKGLGIGVYTGITY 60
 QY 78 YNPGLKSRVITSDTSKNQFSKLSTVADTAVYICAREIAAPRHYE-----D 127
 Db 61 YNPFLRGRVITSDVTSRQFSILNRSMADTAMTCAR---GNPPPYDIDGTGSDSID 117
 QY 128 YMGQGLTVYSS 139
 Db 118 VMGQGTIVHYSS 129

RESULT 3
 HV46_MOUSE STANDARD; PRT; 137 AA.
 AC P01822;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 01-AUG-1992 (Rel. 23, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE IG HEAVY CHAIN V REGION MOPC 315 PRECURSOR.
 OS Mus musculus (Mouse)
 OC Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE; 89238351.
 RA Rinfret A., Horne C., Dorrington K.J., Klein M.;
 RT "Cloning, sequencing and expression of the rearranged MOPC 315 VH
 gene segment.";
 RL Mol. Immunol. 26:431-434(1989).
 RN [2]
 RP SEQUENCE OF 1-31.
 RX MEDLINE; 78094475.
 RA Jilka R.L., Peetka S.;
 RT "Amino acid sequence of the precursor region of MOPC-315 mouse
 immunoglobulin heavy chain.";
 RL Proc. Natl. Acad. Sci. U.S.A. 74:5692-5696(1977).
 RN [3]
 RP SEQUENCE OF 1-21.
 RX MEDLINE; 79148758.
 RA Schechter I., Wolf O., Zemell R., Burstein Y.;
 RT "Structure and function of immunoglobulin genes and precursors.";
 RL Fed. Proc. 38:1839-1845(1979).
 RN [4]
 RP SEQUENCE OF 19-136.
 RX MEDLINE; 74170779.
 RA Francis S.R., Leslie R.G.O., Hood L., Eisen H.N.;

RT "Amino-acid sequence of the variable region of the heavy (alpha)
 RT chain of a mouse myeloma protein with anti-hapten activity.";
 RL Proc. Natl. Acad. Sci. U.S.A. 71:1123-1127(1974).
 RN [5]
 RP REVISION TO 53.
 RX MEDLINE; 77244979.
 RA Hood L., Margolis M.N., Givol D., Zakut R.;
 RT Unpublished results, cited by:
 RL Padlan E.A., Davies D.R., Peck I., Givol D., Wright C.;
 RL Cold Spring Harb. Symp. Quant. Biol. 41:627-637(1977).
 CC -1- MISCELLANEOUS: THIS ALPHA CHAIN WAS ISOLATED FROM A MYELOMA
 CC PROTEIN THAT HAS ANTI-DINITROPHENYL ACTIVITY.
 CC -----
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DR EMBL; M27638; AAA61337.1; -
 DR EMBL; X07880; CAA30727.1; -
 DR PIR; P0102; AVM535.
 DR PFAM; PF00047; 1g; 1.
 KW Immunoglobulin V region; Signal.
 FT SIGNAL 1 18
 FT CHAIN 19 137
 FT DOMAIN 19 48
 FT DOMAIN 49 54
 FT DOMAIN 55 68
 FT DOMAIN 69 84
 FT DOMAIN 85 116
 FT DOMAIN 117 126
 FT DOMAIN 127 137
 FT DISULFID 40 114
 FT CONFLICT 15 15
 FT CONFLICT 15 15
 FT CONFLICT 77 78
 FT CONFLICT 102 102
 FT CONFLICT 123 123
 FT NON_TER 137 137
 SO SEQUENCE 137 AA; 15399 MW; FB3828304C2B81DC CRC64;

Query Match 54.5%; Score 408; DB 1; Length 137;
 Best Local Similarity 60.3%; Pred. No. 1.9e-32;
 Matches 85; Conservative 18; Mismatches 32; Indels 6; Gaps 4;

QY 1 MKHLMPFLLVAPRWLVQVQLQDAGAGLLKPSSETLTCAVYGGSF--SGYWSWIRPP 59
 Db 1 MKVLSILYLTAIP-GIMSDVOQLQESGPGLVKPSOSLSLTCSTGTGITSIGYRWIRPP 59
 QY 60 PGKGLWIGENHSGSTNTPNSLKSRTVITSDTSKNQFSKLSTVADTAVYICAREIA 119
 Db 60 PGKLEWLGFIKYGDSNGVPSLKNRYSITRDSNENQFELKNSVTEDTATYACAGD-- 117
 QY 120 ARPH-REYDYGQGLTVYSS 139
 Db 118 -NDLTYFDYMGQGTIVYSS 137

RESULT 4
 HV2G_HUMAN STANDARD; PRT; 117 AA.
 ID P01825;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 15-JUL-1986 (Rel. 01, Last sequence update)
 DT 21-JUL-1999 (Rel. 38, Last annotation update)
 DE IG HEAVY CHAIN V-II REGION NEMM.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

```

RN [1]
RN SEQUENCE.
RX MEDLINE: 77242302.
RA Poljak R.J., Nakashima Y., Chen B.L., Konigsberg W.:
RT "Amino acid sequence of the VH region of a human myeloma
RL Immunoglobulin (IgG New).";
RL Biochemistry 16:3412-3420(1977).
RN [2]
RP X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS) OF FAB FRAGMENT.
RX MEDLINE: 78066916.
RA Saul F.A., Amzel L.M., Poljak R.J.:
RT "Preliminary refinement and structural analysis of the Fab fragment
RT from human immunoglobulin new at 2.0-A resolution.";
RL J. Biol. Chem. 253:585-597(1978).
CC -I- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM AN IGG1 MYELOMA
CC PROTEIN.
DR PIR: A02100; GIHUNM.
DR PDB: 7FAB; 31-JAN-94.
DR PIR: PF00047; 19; 1.
K Immunoglobulin V region; 3D-structure.
F MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
FT NON_TER 117 117
FT STRAND 3 7
FT TURN 11 12
FT TURN 14 15
FT STRAND 18 25
FT TURN 30 31
FT STRAND 33 39
FT TURN 41 42
FT STRAND 46 51
FT TURN 53 54
FT STRAND 57 59
FT HELIX 61 63
FT TURN 64 66
FT STRAND 67 72
FT TURN 73 76
FT STRAND 77 82
FT HELIX 87 89
FT STRAND 91 98
FT STRAND 104 107
FT STRAND 111 115
SO SEQUENCE 117 AA; 12790 MW; 2DA47B509562D237 CRC64;

Query Match 53.1%; Score 397.5; DB 1; Length 117;
Best Local Similarity 64.2%; Pred. NO. 1.6e-31;
Matches 77; Conservative 19; Mismatches 21; Indels 3; Gaps 1;

20 OVOLOQMGAGLKRPESTLTCAYVGGSGFSGYWSMTROPKGLGEMINHSSTNYN 79
Db 1 OVOLEQSGPLVRSQSLTCTVSGSFSDYITWRQPGKLEWLGIVFYHGISDPT 60

OY 80 PSKSRVTISVDTSKNOFSKLSSTVADTAIVYVCARIRAPRRYDYMGGTLYTVSS 139
Db 61 TPLRSRTVMTVDTSKNOFSKLSSTVADTAIVYVCARIRLA---GCIDVWGSGSLTVYSS 117

RESULT 5
HV60_MOUSE STANDARD; PRT; 116 AA.
AC P18531;
DT 01-NOV-1990 (Rel. 16, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE IG HEAVY CHAIN V REGION M315 PRECURSOR.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-BALB/CJ;
RX MEDLINE: 89279149.
RA Levy N.S., Malplero U.V., Lebecque S.G., Gearhart P.J.;

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RT "Early onset of somatic mutation in immunoglobulin VH genes during
RT the primary immune response.";
RL J. Exp. Med. 169:2007-2019(1989).
DR PIR: J10509; HVWS31.
DR PIR: PF00047; 19; 1.
K Immunoglobulin V region; Signal.
FT SIGNAL 1 18
FT CHAIN 19 116
FT DOMAIN 19 48
FT DOMAIN 49 53
FT DOMAIN 54 67
FT DOMAIN 68 84
FT DOMAIN 85 116
FT DISULFID 40 114
FT NON_TER 116 116
SO SEQUENCE 116 AA; 13095 MW; 4562E03E53DC9E10 CRC64;

Query Match 49.5%; Score 370; DB 1; Length 116;
Best Local Similarity 64.1%; Pred. No. 6.9e-29;
Matches 75; Conservative 15; Mismatches 25; Indels 2; Gaps 2;

OY 1 MKHLMPFLVAPRWYLSQVLOQMGAGLKRPESTLTCAYVGGSGF-SGYWSMTROP 59
Db 1 MKVLSLYLTLAP-GILSDVQLQESGGLVKPSQSLTCSVTGYITSGYVNMTRQF 59

OY 60 PKGGLWIGELNHSSTNYNPSKSRVTISVDTSKNOFSKLSSTVADTAIVYCAR 116
Db 60 PGNKLEWNGYISYDGSNNYNPSKSRVTISVDTSKNOFSKLSSTVADTAIVYCAR 116

RESULT 6
HV43_MOUSE STANDARD; PRT; 144 AA.
AC P01819;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE IG HEAVY CHAIN V REGION MOPC 141 PRECURSOR.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE: 81012133.
RA Sakano H., Maki R., Kurosawa Y., Roeder W., Tonegawa S.:
RT "Two types of somatic recombination are necessary for the generation
RT of complete immunoglobulin heavy-chain genes.";
RL Nature 286:676-683(1980).
CC -I- MISCELLANEOUS: THE SEQUENCE SHOWN IS TRANSLATED FROM A
CC DIFFERENTIATED GENE ISOLATED FROM A MELOMA THAT SECRETES IGG2B.
CC
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CC
DR EMBL: J00491; AAA38121.1;
DR EMBL: V00768; CAA24145.1;
DR PIR: A02094; G2MS14.
DR PIR: PF00047; 19; 1.
KW Immunoglobulin V region; Signal.
FT SIGNAL 1 19
FT CHAIN 20 144
FT NON_TER 144 144
SO SEQUENCE 144 AA; 15759 MW; 8E47A7CB3706D30A CRC64;

Query Match 49.4%; Score 369.5; DB 1; Length 144;
Best Local Similarity 53.5%; Pred. No. 9.9e-29;

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Matches 77; Conservative 21; Mismatches 41; Indels 5; Gaps 2;

OY 1 MKHFWELLVAPRWVLSOVQLOMGAGLKPSETLSITCAVYGSFSGYWSWIRPP 60
 DB 1 MAVTALLFLAFIPSCISOVOLKESGPGLVAPSOSSITCTVSGSLGVNWRPP 60
 OY 61 GGLWEIGINHGSTNPNPSLKSRVTVISVDSKNOFSLKSSVTAADTAAYVCAR---E 117
 DB 61 GGLWEIGINHGSTNPNPSLKSRVTVISVDSKNOFSLKSSVTAADTAAYVCAR---E 117
 OY 118 IAAHRHRY--DYNGOGTLVTVSS 139
 DB 121 YGRSDKFTFLDYWGOGTSTVTVSS 144

RESULT 7

HV47_MOUSE
 ID HV47_MOUSE STANDARD; PRT; 113 AA.

AC 201823;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE IG HEAVY CHAIN V REGION 36-60.
 OS Mus musculus (Mouse).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
 RN [1]
 RP SEQUENCE.
 RX STRAIN-A/J;
 RX MEDLINE; 84024551.
 RA Juzczak E.C., Margolies M.N.;
 RT "Amino acid sequence of the heavy chain variable region from the A/J
 RT mouse anti-arsenate monoclonal antibody 36-60 bearing a minor
 RT idioType."
 RT IdioType."
 RL Biochemistry 22:4291-4296(1983).
 CC -1- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM AN ANTIARSONATE
 CC MONOCLONAL ANTIBODY OF THE IGG2A SUBCLASS. IT REPRESENTS A SECOND
 CC IDIOTYPE FAMILY CHARACTERISTIC OF THE ANTIARSONATE RESPONSE OF
 CC STRAIN A/J MICE.
 CC PIR; A02098; G2MS60.
 DR PFAM; PF00047; 1g; 1.
 DR Immunoglobulin V region: Antiaresonate antibody.
 KW NON_TER 113 113
 FT SEQUENCE 113 AA; 12734 MW; 38DC0EB3F5075B7 CRC64;

Query Match 48.1%; Score 359.5; DB 1; Length 113;
 Local Similarity 59.2%; Pred. No. 6.8e-28;
 Matches 71; Conservative 19; Mismatches 23; Indels 7; Gaps 1;

OY 20 QVQLQMGAGLKPSETLSITCAVYGSFSGYWSWIRPPGKLEWIGELNHGSTNYN 79
 DB 1 EVOIQEGSGPLVRSQSLTSLCTVSGSIISDYNNWIRKFGNKLHMGITISVGSITYN 60
 OY 80 PSLSKRTTVISVDSKNOFSLKSSVTAADTAAYVCAREIARPHRYDYNGOGTLVTVSS 139
 DB 61 PSLSKRSITSDTSKNOFYQLNLSVTSSEDTATYCT-----SLRAVYNGOGTLVTVSA 113

RESULT 8

HV02_XENLA
 ID HV02_XENLA STANDARD; PRT; 135 AA.

AC P20957;
 DT 01-FEB-1991 (Rel. 17, Created)
 DT 01-FEB-1991 (Rel. 17, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE IG HEAVY CHAIN V REGION XIG14 PRECURSOR (FRAGMENT).
 OS Xenopus laevis (African clawed frog).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae;
 RN [1]
 RP SEQUENCE FROM N.A.

RX MEDLINE; 86176921.
 RA Schwager J., Mikoryak C.A., Steiner L.A.;
 RT "Amino acid sequence of heavy chain from Xenopus laevis Igm deduced
 RT from cDNA sequence: implications for evolution of immunoglobulin
 RT domains."
 RL Proc. Natl. Acad. Sci. U.S.A. 85:2245-2249(1988).

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 CC or send an email to license@isb-sib.ch).

DR EMBL; J03632; AAA49791.1;
 DR PIR; B31933; B31933.
 DR PFAM; PF00047; 1g; 1.
 KW Immunoglobulin V region: Signal.
 FT NON_TER 1 1
 FT SIGNAL <1 18
 FT CHAIN 19 135 IG HEAVY CHAIN V REGION XIG14.
 FT NON_TER 135 135
 SO SEQUENCE 135 AA; 15080 MW; EBC467105C00732E CRC64;

Query Match 48.1%; Score 359.5; DB 1; Length 135;
 Best Local Similarity 54.5%; Pred. No. 8.3e-28;
 Matches 73; Conservative 19; Mismatches 39; Indels 3; Gaps 2;

OY 6 FFLVLAAPRWVLSOVQLOMGAGLKPSETLSITCAVYGSFSGYWSWIRPPGKLE 65
 DB 5 FIFMFSPSCISQTLQESGPGTVAPSRSLRITCTVSGFELSSYHMHWRPPGKLE 63
 OY 66 WIGELNHGSTNPNPSLKSRVTVISVDSKNOFSLKSSVTAADTAAYVCAREIARPHRY 125
 DB 64 WIGYIANGSGTALDLSKRVITIKDNGKRVYQLONGMEVKDTAMAYCARAYASGN- 121
 OY 126 FDYWGOGTLVTVSS 139
 DB 122 FDYWGOGTLVTVSS 135

RESULT 9

HV61_MOUSE
 ID HV61_MOUSE STANDARD; PRT; 116 AA.

AC P18532;
 DT 01-NOV-1990 (Rel. 16, Created)
 DT 01-NOV-1990 (Rel. 16, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE IG HEAVY CHAIN V REGION 1B43 PRECURSOR.
 OS Mus musculus (Mouse).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 RN [1]
 RP SEQUENCE FROM N.A.
 RX STRAIN-BALB/CJ;
 RX MEDLINE; 89279149.
 RA Levy N.S., Malipiero U.V., Lebecque S.G., Gearhart P.J.;
 RT "Early onset of somatic mutation in immunoglobulin VH genes during
 RT the primary immune response."
 RL J. Exp. Med. 169:2007-2019(1989).
 CC -1- MISCELLANEOUS: THIS SEQUENCE BELONGS TO THE VH3660 SUBFAMILY.
 CC PIR; J05058; HVS1B.
 DR PFAM; PF00047; 1g; 1.
 KW Immunoglobulin V region: Signal.
 FT SIGNAL 1 18
 FT CHAIN 19 116 IG HEAVY CHAIN V REGION 1B43.
 FT DOMAIN 19 48 FRAMEWORK 1.
 FT DOMAIN 49 53 COMPLEMENTARITY-DETERMINING 1.
 FT DOMAIN 54 67 FRAMEWORK 2.
 FT DOMAIN 68 84 COMPLEMENTARITY-DETERMINING 2.
 FT DOMAIN 85 116 FRAMEWORK 3.

| | | | | |
|--------------------------|--------|--------------------|-----------|-------------|
| Query Match | 45.9%; | Score 343; | DB 1; | Length 116; |
| Best Local Similarity | 60.7%; | Pred. No. 2.7e-26; | | |
| Matches 71; Conservative | 16; | Mismatches 28; | Indels 2; | Gaps 2 |

```
QY      1 MKHLMFELLVLAAPRWVLVSQVOLOOWGAGLLKPSSETLSLTCANYGGSF-SGYWMSIRQP 59
       | : | | : ||||| : ||::||| | | | | | 
Db      1 MRVLILCLFTAFP-GLISDVQLQGSGPDLYKPSQSLSLTCTVTYGSLPNSGSWMHIRQF 59
```

QY 60 PGKGLMEIGELNHGSGSTNYPNSLKSRVTSVDTSKNQFSKLSSVTAADTAVYYCAR 116
|||:::|||||:::|||||:::|||||
Db 60 PGNKLEMGVIHYSGNTSYNPSLSKRSISTRDTSKNQFELQNSVTTEDEPAVYYCAR 116

| | | |
|-----------|------|----|
| RESULT | 10 | |
| HV | 0000 | |
| MOUSE | | |
| ID | 007 | |
| MOUSE | | |
| 00751 | | |
| 00775 | | |
| STANDARD; | | |
| PRT; | 139 | AA |

DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, last sequence update)
DT 15-JUL-1999 (Rel. 38, last annotation update)
DE IG HEAVY CHAIN V REGION B1-8/186-2 PRECURSOR.

OC Eukaryota; Metazoa; Chordata; Cranulata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
RN [1]
RP SEQUENCE FROM N.A.

RX MEDLINE; 81234548.
RA Bothwell A.L.M., Paskind M., Reth M., Imanishi-Kari T., Rajewsky K.,
RA Baltimore D.;
RT "Heavy chain variable region contribution to the NPb family of

CC -1- MISCELLANEOUS: THE B1-8 MU CHAIN MRNA WAS CLONED FROM A HYBRIDOMA MAKING ANTIBODIES TO THE HAPTEN (4-HYDROXY-3-NITROPHENYL)ACETYL (NPB ANTIBODIES).

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DR EMBL: J00529; AAA38170.1; -
DR PIR: A02034; MMS18.
DR PFAM: PF00047; 1g: 1.
KW Immunoglobulin V region; Signal.

| | | | | |
|----|--------|----|-----|-------------------------------------|
| FT | CHAIN | 20 | 139 | IG HEAVY CHAIN V REGION B1-8/186-2. |
| FT | DOMAIN | 20 | 49 | FRAMEWORK 1. |
| FT | DOMAIN | 50 | 54 | COMPLEMENTAITY-DETERMINING 1. |
| FT | DOMAIN | 55 | 68 | FRAMEWORK 2. |

| | | | | |
|----|----------|-----|-----|----------------|
| FT | DOMAIN | 86 | 117 | FRAMEWORK 3. |
| FT | DOMAIN | 118 | 124 | D SEGMENT. |
| FT | DOMAIN | 125 | 139 | JH2 SEGMENT. |
| FT | DISULFID | 41 | 115 | BY SIMILARITY. |

SO SEQUENCE 139 AA; 15419 MW; 1B57DD4FD0C9F465 CRC64;

| | | | | |
|--------------------------|-------|-------------------|-----------|------------|
| Query Match | 44.1% | Score 330 | DB 1 | Length 139 |
| Best Local Similarity | 50.4% | Pred. NO. 5.7e-25 | | |
| Matches 67; Conservative | 22; | Mismatches 42; | Indels 2; | Gaps 2 |

QY 8 LLLVAPRWLSQVOLOQWAGGLKPSETLSLTCAYVGGSGYWSWIRQPPGKLEWI 67

Db

8 LFLAATATGCHSQVQLQPGAEIVKPGASVYKLSCKASGYTFSTWMMHWKQRPGRGLEW

Dy 68 GELN-HSSSTNNPPLKSRVILSDTISKNDPSLKLSTVTAAIDVAHYCCARELNARPHRF 12
| : | | | | | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
68 GRDPHSGGTCKINENFKSKALITVDKPSSTAYMQSLSTSEDSAYYYCAR-YDYGSSTF 12

| | | | |
|----|-----|---------------|-----|
| QY | 127 | DYWGQGTLLTVSS | 139 |
| | | : | |
| Db | 127 | DYWGQGTLLTVSS | 139 |

| RESULT | 11 |
|---------------|---------|
| HV11_MOUSE | |
| ID HV11_MOUSE | |
| AC P01755; | |
| STANDARD; | |
| PRT; | 137 AA. |

```

21-JUL-1986 (Rel. 01, Last sequence update)
21-JUL-1986 (Rel. 01, Created)
15-JUL-1999 (Rel. 38, Last annotation update)
IG HEAVY CHAIN V REGION S43 PRECURSOR.
Mus musculus (Mouse).

```

CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus [1]

RA Botnelli A.L.M., Paskind M., Reth M., Imanishi-Kari T., Rajewsky K., Baltimore D., "Heavy chain variable region contribution to the NPb family of RT cell 34.6/35-637/10831 somatic mutation evident in a gamma 2a variable region.", *Cell* 34:635-637/10831.

CC
CC
CC - THE GAMMA-2A CHAIN KENNA WAS CLONED FROM A HYBRIDOMA
CC MAKING ANTIBODIES TO THE HAPTEN (4-HYDROXY-3-NITROPHENYL)ACETYL
CC (NPB ANTIBODIES).
CC
CC

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CC or send an email to license@isb-sib.ch).

DR EMBL; J00539; AAA38172.1; -.
DR PIR; A02038; G2MS43.
DR PFAM; PF00047; 1g; 1.
KW Immunoglobulin V region; Signal

| FT | CHAIN | 20 | 137 | IG HEAVY CHAIN V REGION S43. |
|----|--------|----|-----|--------------------------------|
| FT | DOMAIN | 20 | 49 | FRAMEWORK 1. |
| FT | DOMAIN | 50 | 54 | COMPLEMENTALITY-DETERMINING 1. |
| FT | DOMAIN | 55 | 68 | FRAMEWORK 2. |

| | | | | |
|----|-----------|-----|-----|----------------|
| FT | DOMAIN | 86 | 117 | FRAMEWORK 3. |
| FT | DOMAIN | 118 | 122 | D SEGMENT. |
| FT | DOMAIN | 123 | 137 | JH2 SEGMENT. |
| FT | DISULEFID | 41 | 115 | BY SIMILARITY. |

```

SO      NON-LEN  22  137
SEQUENCE 137 AA: 15200 MW:  ADD5881BF44B8EC9 CRC64

Query Match  44.0%:  Score 329:  DR 1: 1e6nt

```

| | | | | |
|--------------------------|-------|-----------------|-------|-------------------|
| Query Match Similarity | 44.0% | Score 329; | DB 1; | Length 137; |
| Best Local Similarity | 49.6% | Pred. NO.7e-25; | | |
| Matches 66; Conservative | 22; | Mismatches | 41; | Indels 4; Gaps 2; |

QY 8 LLVAPRWLSQVQLQWGAGLLKPSSETLSLTCAVYGGSFSGYYWSMIRQPPCKGLEMI 67

[illegible]

00 UNLDFN03011NENF N0001111UNFSSIAIMQUBSSBISBSAVIICAK--1XKGRIF 12

QY 127 DYMGGTLTVSS 139
 ||||| :|||
 DB 125 DYMGGTLTVSS 137

RESULT 12
 HV37_MOUSE

ID HV37_MOUSE STANDARD; PRT; 119 AA.

AC P01807;

DT 21-JUL-1986 (Rel. 01, Created)

DT 21-JUL-1986 (Rel. 01, Last sequence update)

DE IG HEAVY CHAIN V REGION X44.

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

RN [1]

RP SEQUENCE.

RY MEDLINE; 79223895.

RA Rao D.N., Rudnikoff S., Krutzsch H., Potter M.;

RT "Structural evidence for independent joining region gene in

RT its potential role in generating diversity in

RT complementarity-determining regions."

RL Proc. Natl. Acad. Sci. U.S.A. 76:2890-2894 (1979).

CC -1- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM AN IGA MYELOMA PROTEIN

CC THAT BINDS GALACTAN.

DR HSSP; P01810; 2FBU.

DR PFAM; PF00047; 19; 1.

KW Immunoglobulin V region.

FT NON_TER 119

SO SEQUENCE 119 AA; 13246 MW; BC34FCBF31CD41B3 CRC64;

Query Match 43.98; Score 328; DB 1; Length 119;

Best Local Similarity 54.58; Pred. No. 7.5e-25;

Matches 66; Conservative 17; Mismatches 34; Indels 4; Gaps 2;

QY 20 OYLOOMGAGILKPSLTLTCAVYGGSGFYWMSIRQPPKGLMEIGHSGST-NY 78

DB 1 EYKLEGGGLVOPGSGSLTSCAASGDFSRWMSVWROAPKGLMEIGHSGSTINY 60

QY 79 NPSLKRVTISVDTSKNOFSLKSLSYTAADTAAYVCARETIARPHRFYDYGOGTLTVS 138

DB 61 TPLKCKFIISDNKNTLYLQMSKVSSEDTALTYCAR---LHYGIAAHGGTLTVS 117

QY 39 S 139

DB 118 A 118

RESULT 13

HV62_MOUSE

ID HV62_MOUSE STANDARD; PRT; 117 AA.

AC P18533;

DT 01-NOV-1990 (Rel. 16, Created)

DT 01-NOV-1990 (Rel. 16, Last sequence update)

DT 15-JUL-1999 (Rel. 38, Last annotation update)

DE IG HEAVY CHAIN V REGION 733 PRECURSOR.

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

RN [1]

RP SEQUENCE FROM N.A.

RX STRAIN-BALB/CJ.

RE MEDLINE; 89279149.

RT "Early Onset of somatic mutation in immunoglobulin VH genes during

RT the primary immune response."

RT J. Exp. Med. 169:2007-2019 (1989).

DR PIR; J10510; HVMS73.

DR PFAM; PF00047; 19; 1.

KW Immunoglobulin V region; signal.
 FT SIGNAL 1 18
 FT CHAIN 19 117 IG HEAVY CHAIN V REGION 733.
 FT DISULFID 40 115 BY SIMILARITY.
 FT NON_TER 117 117
 SO SEQUENCE 117 AA; 13223 MW; 1595517827F976BE CRC64;

Query Match 43.68; Score 326.5; DB 1; Length 117;
 Best Local Similarity 57.68; Pred. No. 1e-24;
 Matches 68; Conservative 15; Mismatches 32; Indels 3; Gaps 2;

QY 1 MKHLMPELLVAAPRWLSOVLOOMGAGILKPSLTLTCAVYGGSGF--GYWMSIRQ 58

DB 1 MKHFTLLYLTVP--GILSDVQDESGLPQSPQSTALCTVTGISTGNRWMSIRQ 59

QY 59 PGKGLMEIGHSGSTINYNPSLKRVTISVDTSKNOFSLKSLSYTAADTAAYVCAR 116

DB 60 FPGKLEWIGIYYSALTSYNPSKSRVTITRTDTSKNOFLEHNSLTAEDTATYCAR 117

RESULT 14

HV38_MOUSE

ID HV38_MOUSE STANDARD; PRT; 119 AA.

AC P01808;

DT 21-JUL-1986 (Rel. 01, Created)

DT 21-JUL-1986 (Rel. 01, Last sequence update)

DT 15-JUL-1999 (Rel. 38, Last annotation update)

DE IG HEAVY CHAIN V REGION T601.

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

RN [1]

RP SEQUENCE.

RY MEDLINE; 79223895.

RA Rao D.N., Rudnikoff S., Krutzsch H., Potter M.;

RT "Structural evidence for independent joining region gene in

RT immunoglobulin heavy chains from anti-galactan myeloma proteins and

RT its potential role in generating diversity in

RT complementarity-determining regions."

RL Proc. Natl. Acad. Sci. U.S.A. 76:2890-2894 (1979).

CC -1- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM AN IGA MYELOMA PROTEIN

CC THAT BINDS GALACTAN.

DR HSSP; P01810; 2FBU.

DR PFAM; PF00047; 19; 1.

KW Immunoglobulin V region.

FT NON_TER 119

SO SEQUENCE 119 AA; 13169 MW; BC38CC84E6EA00E8 CRC64;

Query Match 43.68; Score 326; DB 1; Length 119;

Best Local Similarity 54.58; Pred. No. 1.2e-24;

Matches 66; Conservative 16; Mismatches 35; Indels 4; Gaps 2;

QY 20 OYLOOMGAGILKPSLTLTCAVYGGSGFYWMSIRQPPKGLMEIGHSGST-NY 78

DB 1 EYKLEGGGLVOPGSGSLTSCAASGDFSRWMSVWROAPKGLMEIGHSGSTINY 60

QY 79 NPSLKRVTISVDTSKNOFSLKSLSYTAADTAAYVCARETIARPHRFYDYGOGTLTVS 138

DB 61 TPLKCKFIISDNKNTLYLQMSKVSSEDTALTYCAR---LGYGYFPWAGTLTVS 117

QY 139 S 139

DB 118 S 118

RESULT 15

HV40_MOUSE

ID HV40_MOUSE STANDARD; PRT; 119 AA.

AC P01810;

DT 21-JUL-1986 (Rel. 01, Created)

DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE IG HEAVY CHAIN V REGION J539.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
RN [1]
RP PRELIMINARY SEQUENCE.
RX MEDLINE; 79223895.
RA Rao D.N., Rudikoff S., Krutzsch H., Potter M.;
RT "Structural evidence for independent joining region gene in
immunoglobulin heavy chains from anti-galactan myeloma proteins and
its potential role in generating diversity in
complementarity-determining regions.";
RN Proc. Natl. Acad. Sci. U.S.A. 76:2890-2894(1979).
RP [2]
RX X-RAY CRYSTALLOGRAPHY (2.6 ANGSTROMS).
RA Medline; 88217852.
RA Suh S.W., Bhat T.N., Navia M.A., Cohen G.H., Rao D.N., Rudikoff S.,
RA Davies D.R.;
RT "The galactan-binding immunoglobulin Fab J539: an X-ray diffraction
study at 2.6-A resolution.";
RL Proteins 1:74-80(1986).
CC -I- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM A MYELOMA PROTEIN THAT
CC BINDS GALACTAN.
CC PIR: A02080; AVMSJ5.
DR PDB: 2FBJ; 15-OCY-90.
DR PIR: A02080; AVMSJ5.
RW Immunoglobulin V region; 3D-structure.
FT NON_TER 119 119
FT STRAND 3 7
FT STRAND 10 12
FT TURN 14 15
FT STRAND 18 25
FT STRAND 29 31
FT HELIX 34 39
FT TURN 41 42
FT STRAND 45 51
FT TURN 53 54
FT STRAND 58 60
FT TURN 62 67
FT STRAND 68 72
FT STRAND 78 83
FT HELIX 88 90
FT STRAND 92 100
FT TURN 101 103
FT STRAND 104 108
FT STRAND 112 116
FT SEQUENCE 119 AA; 13240 MW; 577BAF1DB675C1F1 CRC64;

Query Match 43.4%; Score 325; DB 1; Length 119;
Best Local Similarity 53.7%; Pred. No. 1.4e-24;
Matches 65; Conservative 19; Mismatches 33; Indels 4; Gaps 2;

OY 20 OYOLQWGMGLKPGSETSLTCAYVGGSGYVSMIRPGKGLWIGELN-HSGSTNY 78
DB 1 EYKLESGGGLVOPGSLKSCAAGFDPSKYMSKVRQAPGKGLWIGELNHPDSGITNY 60
OY 79 NPSLKRVTISYDTSKNOFSLKLSVTADTAIVYCCAREIARPHRYEDYMGQGLTVYS 138
DB 61 TPLSLDKRFLISHDNKNSLYLQMSKVRSEDTALYCAR---LHYGYNAVMQGLTVYS 117
OY 139 S 139
DB 118 A 118

Search completed: July 26, 2000, 14:25:25
Job time: 1331 sec

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RESULT 2
ID 075725 PRELIMINARY; PRT; 82 AA.
AC 075725;
DT 01-NOV-1998 (TREMblrel. 08, Created)
DT 01-NOV-1998 (TREMblrel. 08, Last sequence update)
DT 01-NOV-1999 (TREMblrel. 12, Last annotation update)
DE IG HEAVY CHAIN VARIABLE REGION (FRAGMENT).
GN VH.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Primates; Catarrhini; Homiidae; Homo.
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-INTERESTINE;
RA FISCHER M., KUEPPERS R.;
RT Human Iga and Igm secreting intestinal plasma cells carry heavily
mutated VH region genes."
RL Submitted (JUL-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL: A0009532; CA08729.1; -.
DR HSSP: P01825; 7FAB. 1
FT NON_TER 1
FT NON_TER 82
SQ SEQUENCE 82 AA; 9566 MW; 1F2E1379 CRC32;

Query Match 43.9%; Score 328.5; DB 4; Length 82;
Best Local Similarity 74.4%; Pred. No. 1.3e-26;
Matches 61; Conservative 7; Mismatches 13; Indels 1; Gaps 1;

OY 49 SGYWSMIRPPGKGLWIGINHSSTNYPKSLKRYTISVDTSKNOFSLKSSVTAAAD 108
Db 1 SREYWGIRPPGKGLWIGINHSSTNYPKSLKRYTISVDTSKNOFSLKSSVTAAAD 60
OY 109 TAVYVCAREI-AARPHRYFDY 129
Db 61 TAVYVCAREI-AARPHRYFDY 82

RESULT 3
ID 075739 PRELIMINARY; PRT; 78 AA.
AC 075739;
DT 01-NOV-1998 (TREMblrel. 08, Created)
DT 01-NOV-1998 (TREMblrel. 08, Last sequence update)
DT 01-NOV-1998 (TREMblrel. 08, Last annotation update)
DE 3 HEAVY CHAIN VARIABLE REGION (FRAGMENT).
GN VH.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Primates; Catarrhini; Homiidae; Homo.
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-INTERESTINE;
RA FISCHER M., KUEPPERS R.;
RT Human Iga and Igm secreting intestinal plasma cells carry heavily
mutated VH region genes."
RL Submitted (JUL-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL: A0009538; CA08743.1; -.
FT NON_TER 1
FT NON_TER 78
SQ SEQUENCE 78 AA; 9031 MW; 05D273B9 CRC32;

Query Match 41.7%; Score 312; DB 4; Length 78;
Best Local Similarity 74.4%; Pred. No. 5.8e-25;
Matches 58; Conservative 8; Mismatches 12; Indels 0; Gaps 0;

OY 52 YWSMIRPPGKGLWIGINHSSTNYPKSLKRYTISVDTSKNOFSLKSSVTAAADTAV 111
Db 1 YWSMIRPPGKGLWIGINHSSTNYPKSLKRYTISVDTSKNOFSLKSSVTAAADTAV 60

OY 112 YVCAREIAARPHRYFDY 129
Db 61 YVCAREIAARPHRYFDY 78

RESULT 4
ID 095509 PRELIMINARY; PRT; 147 AA.
AC 095509;
DT 01-NOV-1999 (TREMblrel. 12, Created)
DT 01-NOV-1999 (TREMblrel. 12, Last sequence update)
DT 01-NOV-1999 (TREMblrel. 12, Last annotation update)
DE VH3 PROTEIN (FRAGMENT).
GN VH3.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Primates; Catarrhini; Homiidae; Homo.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE: 96071149.
RA CAO J., VESCTO R.A., RETTIG M.B., HONG C.H., KIM A., LEE J.C.,
LICHENSTEIN A.K., BERENSON J.R.;
RT "A CD10-positive subset of malignant cells is identified in multiple
myeloma using PCR with patient-specific immunoglobulin gene primers."
RL Leukemia 9:1948-1953(1995).
DR EMBL: S80860; AAD14339.1; -.
FT NON_TER 1
FT NON_TER 147
SQ SEQUENCE 147 AA; 15768 MW; BDD8F70 CRC32;

Query Match 40.6%; Score 304; DB 4; Length 147;
Best Local Similarity 48.1%; Pred. No. 8.1e-24;
Matches 63; Conservative 20; Mismatches 32; Indels 16; Gaps 3;

OY 20 QVQLQDQWAGLILPSELTSLTCAVYGSFSGYWSMIRPPGKGLWIGINHSSTNYP 79
Db 1 QVHLVESGGGVQPGKSLRSCASGFTSTYGMNWRQAPGGLWVALLISYDGSYQY 60
OY 80 P-SLKSRYTISVDTSKNOFSLKSSVTAAADTAVYVCAREIAARPHRYF-----DY 128
Db 61 AGSVKGRFTISRDNSKNTLYLQMTSLRVEDTAVYCAKD-----GNYPFSGVGYRAGIDY 115
OY 129 WGGGLTVTVSS 139
Db 116 WGGGLTVTVSS 126

RESULT 5
ID 075743 PRELIMINARY; PRT; 75 AA.
AC 075743;
DT 01-NOV-1998 (TREMblrel. 08, Created)
DT 01-NOV-1998 (TREMblrel. 08, Last sequence update)
DT 01-NOV-1998 (TREMblrel. 08, Last annotation update)
DE IG HEAVY CHAIN VARIABLE REGION (FRAGMENT).
GN VH.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Primates; Catarrhini; Homiidae; Homo.
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-INTERESTINE;
RA FISCHER M., KUEPPERS R.;
RT Human Iga and Igm secreting intestinal plasma cells carry heavily
mutated VH region genes."
RL Submitted (JUL-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL: A0009543; CA08747.1; -.
FT NON_TER 1
FT NON_TER 75
SQ SEQUENCE 75 AA; 8667 MW; 8D5C330F CRC32;

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Query Match Summary      39.6%; Score 296.5; DB 4; Length 75;
Best Local Similarity   71.8%; Pred. No. 2,1e+23;
Matches 56; Conservative 6; Mismatches 13; Indels 3; Gaps 11

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OY 52 YWSWIRPPGKGLWIGELINHSNSTNYNSLSKRYTISVDTSKNOFSLKSYTADTAV 111
Db 1 YWATIRPPGKGLWIGELINHSNSTNYNSLSKRYTISVDTSKNOFSLKSYTADTAV 60
OY 112 YYCAREIARPHRYFDYV 129
Db 61 YYCARR---HGYSWEDPW 75

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RESULT 6
OY921C4 PRELIMINARY; PRT; 118 AA.
O921C4
AC O921C4;
DT 01-MAY-1999 (TREMBlrel. 10, Created)
DT 01-MAY-1999 (TREMBlrel. 10, Last sequence update)
DT 01-MAY-1999 (TREMBlrel. 10, Last annotation update)
Db 01-MAY-1999 (TREMBlrel. 10, Last annotation update)
OY ANTI-PORCINE VCAM MAB 3F4 HEAVY CHAIN VARIABLE REGION (FRAGMENT).
O Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Rodentia; Sclurognathi; Muridae; Murinae; Mus.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-BALB/C;
RA MUELLER J.P., GIANNONI M.A., HARTMAN S.T., ELLIOTT E.A., SOUINTO S.P.,
RA MATIS L.M., EVANS M.J.;
RT "Humanized porcine VCAM-specific monoclonal antibodies with chimeric
RT 19g2/64 constant regions block human leukocyte binding to porcine
RT endothelial cells."
RL Submitted (NOV-1996) to the EMBL/GenBank/DBJ databases.
DR EMBL; U78801; AAD00293.1; -.
FT NON-TER 1 118
FT NON-TER 1 118
SO SEQUENCE 118 AA; 13036 MW; 45653221 CRC32;

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Query Match      38.4%; Score 287; DB 11; Length 118;
Best Local Similarity 45.5%; Pred. No. 3,4e+22;
Matches 55; Conservative 23; Mismatches 39; Indels 4; Gaps 2

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OY 20 OYOLOQMGAGLKPSETSLTCAVYGGSGYWSNIRPPGKGLWIGELI-NHSGSTNY 78
Db 1 OYOQOAGSGLARPMASVYKLSKASGYNNNSYWMQVQKPGGGLWIGELIAYIPGDDTGY 60
OY 79 NPSLSRYTISVDTSKNOFSLKSYTADTAVYYCAREIARPHRYFDYWGGLTYVS 138
Db 61 TOKFPGKATLTADKSSSTAYMOLSLSPASDSAYVCARRTVG---GYFDYWGGLTYVS 117
OY 139 S 139
Db 118 S 118

```

```

RESULT 7
ID 075737 PRELIMINARY; PRT; 88 AA.
O75737
AC 075737;
DT 01-NOV-1998 (TREMBlrel. 08, Created)
DT 01-NOV-1998 (TREMBlrel. 08, Last sequence update)
DT 01-NOV-1998 (TREMBlrel. 12, Last annotation update)
DE VH HEAVY CHAIN VARIABLE REGION (FRAGMENT).
GN
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Primates; Catarrhini; Homiidae; Homo.
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-INTESTINE;
RA FISHER M., KUEPPERS R.;
RT "Human Iga and Igm secreting intestinal plasma cells carry heavily

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RT      mutated YH region genes."
RL      Submitted (JUL-1998) to the EMBL/GenBank/DBJ databases.
DR      EMBL; AJ009535; CAA08741.1; -.
DR      HSSP; P01825; 7FAB.
FT      NON_TER
FT      NON_TER
SO      SEQUENCE      88 AA; 10088 MW; C76DC923 CRC32;

Query Match
Best Local Similarity      37.2%; Score 278.5; DB 4; Length 88;
Matches      53; Conservative      11; Mismatches      14; Indels      9; Gaps      2

OY      52 YMSWRPQPGKGLGEMIGTGINHSGSTNNPDLKSRVTISVDTSKNQFSLKSSVTADNAV 111
      ::::|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      2 WMTWVRQAPGRGLGEMIGTGYGGDITNNPDLKGRLTLLDKSMQFSLIRSVTADNAV 61

OY      112 YYCARE-----IAAPHRYE----DYW 129
      |||||      |:::|      |
Db      62 YYCARGGGRHCGIGGRCRYTNGVDYW 88

RESULT      8
O921C6      PRELIMINARY; PRT; 117 AA.
AC      O921C6;
DT      01-MAY-1999 (TREMblrel. 10, Created)
DT      01-MAY-1999 (TREMblrel. 10, Last sequence update)
DT      01-MAY-1999 (TREMblrel. 10, Last annotation update)
DE      ANTI-PORCINE VCAM MAB 2A2 HEAVY CHAIN VARIABLE REGION (FRAGMENT).
OS      Mus musculus (Mouse).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC      Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
[1]
RP      SEQUENCE FROM N.A.
RC      STRAIN-BALB/C;
RA      MOELLER J.P., GIANNONI M.A., HARTMAN S.L., ELLIOTT E.A., SQUINTO S.P.,
RA      MATIS L.M., EVANS M.J.;
RT      "Humanized porcine VCAM-specific monoclonal antibodies with chimeric
RT      IgG2/64 constant regions block human leukocyte binding to porcine
RT      endothelial cells."
RL      Submitted (NOV-1996) to the EMBL/GenBank/DBJ databases.
DR      EMBL; U78799; AAD00291.1; -.
FT      NON_TER
FT      NON_TER
SO      SEQUENCE      117 AA; 13122 MW; DC234181 CRC32;

Query Match
Best Local Similarity      36.0%; Score 269.5; DB 11; Length 117;
Matches      55; Conservative      23; Mismatches      37; Indels      7; Gaps      3;

OY      20 QYOLOQMWAGLLKRPETLSLNCAYVGGSGFYGMWINQPPKQGLGEMIGTINHSQS-TNY 78
      |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      1 QYOLOQSGPOLVPRPTSTVAKISCKAGSYFTSYMMWVNRQPEODLEIMDPSSSEVL 60

OY      79 NPSLSRYTISVDTSKNQFSLKSSVTADNAVYYCAR-ELIARPHRYDYGGGGLTV 137
      |:::|:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      61 NQRLDKAILIYDKSNSNAYVMQFSPISDSAVYICTRGEVS-----WFAVGGGGLTV 115

OY      138 SS 139
      |:
Db      116 SA 117

RESULT      9
O9Y298      PRELIMINARY; PRT; 150 AA.
AC      O9Y298;
DT      01-NOV-1999 (TREMblrel. 12, Created)
DT      01-NOV-1999 (TREMblrel. 12, Last sequence update)
DT      01-NOV-1999 (TREMblrel. 12, Last annotation update)
DE      IGG VH PROTEIN PRECURSOR (FRAGMENT).

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GN IGG VH.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
 CC Eutheria; Primates; Catarrhini; Homidae; Homo.
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE: 9832215.
 RA JACQUEMIN M.G., VANDER ELST L.P.L.;
 RT "Mechanism and kinetics of factor VIII inactivation: study with an
 RT IgG4 monoclonal antibody derived from a hemophilia A patient with
 RT inhibitor".
 RL Blood 92:496-506(1999).
 DR EMBL: AJ224083; CA11829.1; -.
 KW Signal.
 FT SIGNAL.
 FT NON_TER
 SQ SEQUENCE 150 AA; 16031 MW; B18EC39A CRC32;

Query Match
 Best Local Similarity 35.4%; Score 264.5; DB 4; Length 150;
 Matches 61; Conservative 21; Mismatches 53; Indels 5; Gaps 3;

OY 1 MKHLWPELLVAAPRWVLSQVLOQWAGILKPSSETLTCAYVGGSGFYWMTIRPP 60
 DB 1 MDMTRILFLVAAGTGTNAQVLOVSGAEVKKPGASVKKVSGYTLTLPVHWGAP 60
 OY 61 GKLEWIGEIN-HSGSTNPNLSKRVTSVDSKNOFSLKXSSVAAADTAVYCCARETA 119
 DB 61 GKLEWGFDESGESGSIARFQGSVYMTADTSDIAYMELSLKSDDTAVYCCA---V 117
 OY 120 ARPHRFDMYGGGTLYTVSS 139
 DB 118 PDPDA-FDIMGGGTMYTVSS 136

RESULT 10
 ID 095978 PRELIMINARY; PRT; 157 AA.
 AC 095978;
 DT 01-MAY-1999 (TREMblrel. 10, Created)
 DT 01-MAY-1999 (TREMblrel. 10, Last sequence update)
 DE 01-MAY-1999 (TREMblrel. 10, Last annotation update)
 DE VH1 PROTEIN PRECURSOR (FRAGMENT).
 GN VH1.
 OS Homo sapiens (Human).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
 CC Eutheria; Primates; Catarrhini; Homidae; Homo.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE-PERIPHERAL BLOOD;
 RA JOX A., ZANDER T., KUEPPERS R., IRSCH J., KANZLER H., KORNACKER M.,
 RA BOHLEN H., DIEHL V., WOLF J.;
 RT "Absence of immunoglobulin in Hodgkin-Reed Sternberg cells of a
 RT patient with mixed cellularly Hodgkin's disease is associated with
 RT somatic mutations within the untranslated regions of rearranged and
 RT class switch recombined Ig genes".
 RL Submitted (APR-1998) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AJ005570; CA06599.1; -.
 KW Signal.
 FT SIGNAL.
 FT NON_TER
 SQ SEQUENCE 157 AA; 17304 MW; 88468024 CRC32;

Query Match
 Best Local Similarity 34.3%; Score 256.5; DB 4; Length 157;
 Matches 61; Conservative 19; Mismatches 58; Indels 3; Gaps 3;

OY 1 MKHLWPELLVAAPRWVLSQVLOQWAGILKPSSETLTCAYVGGSGFYWMTIRPP 59
 DB 1 MDMTRILFLVAAGTGTNAQVLOVSGAEVKKPGASVKKVSGYTLTLPVHWGAP 59

OY 60 PKGLEWIGEINHS-GSTNPNLSKRVTSVDSKNOFSLKXSSVAAADTAVYCCARETA 118
 DB 60 PKGLEWGFDESGESGSIARFQGSVYMTADTSDIAYMELSLKSDDTAVYCCA---V 117
 OY 119 ARPHRFDMYGGGTLYTVSS 139
 DB 120 ARPHRFDMYGGGTLYTVSS 140

RESULT 11
 ID 043234 PRELIMINARY; PRT; 97 AA.
 AC 043234;
 DT 01-JUN-1998 (TREMblrel. 06, Created)
 DT 01-JUN-1998 (TREMblrel. 06, Last sequence update)
 DE 01-MAY-1999 (TREMblrel. 10, Last annotation update)
 DE RHEUMATOID FACTOR RF-ET13 (FRAGMENT).
 OS Homo sapiens (Human).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
 CC Eutheria; Primates; Catarrhini; Homidae; Homo.
 RN [1]
 RP SEQUENCE FROM N.A.
 RA BORETZEN M., NATVIG J.B., THOMPSON K.M.;
 RA Mol. Immunol. 0:0-0(1997).
 DR EMBL: AF035802; AAB8534.1; -.
 DR PFMV: PF00047; 19; 1.
 FT NON_TER
 FT NON_TER
 SQ SEQUENCE 97 AA; 10748 MW; EC95D20C CRC32;

Query Match
 Best Local Similarity 32.8%; Score 245; DB 4; Length 97;
 Matches 50; Conservative 16; Mismatches 28; Indels 2; Gaps 1;

OY 23 LQWAGILKPSSETLTCAYVGGSGFYW--SWIRPPKGLEWIGEINHSSTNPNP 80
 DB 2 LKESGPAVKNPTLTLTLCVSGFSLNRKGVSWIRPPKRAVEMLAHIFANDEKSI 61
 OY 81 SKSRVTSVDSKNOFSLKXSSVAAADTAVYCCARETA 116
 DB 62 SKSRVTSVDSKNOFSLKXSSVAAADTAVYCCARETA 97

RESULT 12
 ID 075741 PRELIMINARY; PRT; 77 AA.
 AC 075741;
 DT 01-NOV-1998 (TREMblrel. 08, Created)
 DT 01-NOV-1998 (TREMblrel. 08, Last sequence update)
 DT 01-NOV-1999 (TREMblrel. 12, Last annotation update)
 DE IG HEAVY CHAIN VARIABLE REGION (FRAGMENT).
 GN VH.
 OS Homo sapiens (Human).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
 CC Eutheria; Primates; Catarrhini; Homidae; Homo.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE-INTESTINE;
 RA FISCHER M., KUEPPERS R.;
 RT "Human Iga and Igm secreting intestinal plasma cells carry heavily
 RT mutated VH region genes".
 RL Submitted (JUL-1998) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AJ009540; CA08745.1; -.
 DR HSSP: P01772; 2162.
 FT NON_TER
 FT NON_TER
 SQ SEQUENCE 77 AA; 8734 MW; 1F7F9E8E CRC32;

Query Match
 Best Local Similarity 30.0%; Score 224.5; DB 4; Length 77;
 Matches 48; Conservative 6; Mismatches 16; Indels 11; Gaps 3;

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OY 54 SWIRPPKPGKGEIENIHSSG-S-TNYNSLTSRTIYSDSKNOFSKLSSTPAADAVY 11
Db 3 SWNRAPKPGKGLEWMSGISGSDITYYADSVAGRTTISRDNKSNLTSLQNSVTADTAVY 62
OY 113 YCAREIARPHRY----FDY 129
Db 63 YCAR-----HYDSDSPDYW 77

RESULT 13
OY 075730 PRELIMINARY; PRT; 78 AA.
AC 075730:
DT 01-NOV-1998 (TREMblrel. 08, Created)
DT 01-NOV-1998 (TREMblrel. 08, Last sequence update)
DT 01-NOV-1999 (TREMblrel. 12, Last annotation update)
DE IG HEAVY CHAIN VARIABLE REGION (FRAGMENT).
GN VH.
OC Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Primates; Catarrhini; Hominiidae; Homo.
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=INTESTINE.
RA FISCHER M., KUEPPERS R.;
RT "Human Iga and Igm secreting intestinal plasma cells carry heavily
RT mutated VH region genes."
RL Submitted (JUL-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ009527; CAA08734.1; -.
DR HSSP; P01772; 2IG2.
FT NON_TER 1 1
FT NON_TER 80 80
FT NON_TER 1 1
SQ SEQUENCE 78 AA; 8994 MW; 0A38F0E5 CRC32;

Query Match 28.9%; Score 216.5; DB 4; Length 78;
Best Local Similarity 49.4%; Pred. No. 3,2e-15;
Matches 40; Conservative 16; Mismatches 20; Indels 5; Gaps

OY 50 GYWSMINPPGKGLEWNGEINHSSSTN-YNPSLKSRITISVDPSKNOFSKLSSTPAAD 108
Db 2 GYWSWNRAPKPGKGLEWVANINNEGSGKYADSVAGRTTILRDSAKNSLFLQNTLRAED 61
OY 109 TAVYYCAREIARPHRYEDYW 129
Db 62 TAVYHCARDY-----NGHFDYW 78

RESULT 14
OY 075727 PRELIMINARY; PRT; 80 AA.
AC 075727:
DT 01-NOV-1998 (TREMblrel. 08, Created)
DT 01-NOV-1998 (TREMblrel. 08, Last sequence update)
DT 01-NOV-1999 (TREMblrel. 12, Last annotation update)
DE IG HEAVY CHAIN VARIABLE REGION (FRAGMENT).
GN VH.
OC Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Primates; Catarrhini; Hominiidae; Homo.
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=INTESTINE.
RA FISCHER M., KUEPPERS R.;
RT "Human Iga and Igm secreting intestinal plasma cells carry heavily
RT mutated VH region genes."
RL Submitted (JUL-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ009524; CAA08731.1; -.
DR HSSP; P01772; 2IG2.
FT NON_TER 1 1
FT NON_TER 80 80
FT NON_TER 1 1
SQ SEQUENCE 80 AA; 9351 MW; 63DE158A CRC32;

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Query Match          27.8%; Score 208; DB 4; Length 80;
Best Local Similarity 51.9%; Pred. No. 2,4e-14;
Matches 42; Conservative 10; Mismatches 25; Indels 4; Gaps 2

QY 52 YWSMIRPPGKGLEWIGELIN--HSGSTNYNSLSKRVITISVTSKQFSLKLSVTAAAD 108
   | : | | | | | | | | | | : | : | | | | | | | | | : | | |
DB 1 YMDWVRQAPGKGLEWVGGRRKKANSYTTEPYASVSGRFTISRDSDKNSLYLQMSLKTDD 60
QY 109 TAVYTCARIEIARPHRYEDYW 129
   | | | | | | | | | | | | | |
DB 61 TAVYTCARD-HLRSAYEDLW 80

RESULT 15
ID 075729 PRELIMINARY; PRT; 82 AA.
AC 075729;
DT 01-NOV-1998 (TREMBLrel. 08, Created)
DT 01-NOV-1998 (TREMBLrel. 08, Last sequence update)
DT 01-NOV-1999 (TREMBLrel. 12, Last annotation update)
DE IG HEAVY CHAIN VARIABLE REGION (FRAGMENT).
GN VH.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Primates; Catarrhini; Homiidae; Homo.
NC (1)
NM RP SEQUENCE FROM N.A.
RC TISSUE=INTESTINE;
RT FISHER M., KUEPPERS R.;
RA "Human Iga and Igm secreting intestinal plasma cells carry heavily
RL mutated VH region genes.";
RL Submitted (JUL-1998) to the EMBL/Genbank/DBJ databases.
DR EMBL; AJ009526; CAA08733.1; -.
DR HSSP; P01772; 2IG2.
FT NON-TER 1
FT NON-TER 82
SQ SEQUENCE 82 AA; 9396 MW; 9063B32A CRC32;

Query Match          27.2%; Score 203.5; DB 4; Length 82;
Best Local Similarity 50.0%; Pred. No. 7.2e-14;
Matches 41; Conservative 12; Mismatches 26; Indels 3; Gaps 2

QY 51 YWSMIRPPGKGLEWIGELINSG-STNNPPLSKSVITISVTSKQFSLKLSVTAAADT 109
   | : | | | | | | | | | | : | : | | | | | | | | | : | | |
DB 1 YMSWVRQAPGKGLEWVSSIDAGIDITYAESVKGRTISRDNKNTLYLQNTLRAEDT 60
QY 110 AVYICARE--IARPHRYEDYW 129
   | | | | | | | | | | | | | |
DB 61 AVYICVKDGSANSVWDYFDYW 82

```

Search completed: July 26, 2000, 14:25:01
Job time: 1412 sec

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Query Match 27.2%: Score 203.5; DB 4; Length 82;
Best Local Similarity 50.0%: Pred. No. 7,2e-14;
Matches 41; Conservative 12; Mismatches 26; Indels 3; Gaps 2

QY 51 YVMSWIRDPGKGLEWIGETINHS-STNTNPSLKSRTTISVDTSKNQFSLKTSVTADT 109
      |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::|
DB 1 YAMSWVRQAPGKGLEWVSSIDAGIDITYAESVKGRRFTISRDNKNTLYLQWNTLRADT 60
      |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::|

QY 110 AVYYCARE--IAARPHRYFDY 129
      |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::|
DB 61 AVYYCVKDGVSANSWMDYFDY 82
      |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::|

Search completed: July 26, 2000, 14:25:01
Job time: 1412 sec

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GenCore version 4.5
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OM protein - protein search, using sw model

Run on: July 26, 2000, 14:01:26 ; Search time 33.21 Seconds

(without alignments)
83.447 Million cell updates/sec

Title: US-09-203-768a-4
Perfect score: 615

Sequence: 1 LMLPDTTGEIVMTQSPATLS.....QYNWMPYTFGQTKLEIKR 117

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 188963 seqs, 23686106 residues

Minimum DB seq length: 0
Maximum DB seq length: 1000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database: A_Geneseq_36.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|-------|-------------|--------|----------|--------------------|
| 1 | 538.5 | 87.6 | 234 | 1 R52951 | Human anti-IgE MAb |
| 2 | 523 | 85.0 | 129 | 1 R38672 | VK325-Jk2. DNA seq |
| 3 | 518 | 84.2 | 117 | 1 W47582 | Human monoclonal a |
| 4 | 513.5 | 83.5 | 349 | 1 R12128 | 1B1 IgG aberrant 1 |
| 5 | 513.5 | 83.5 | 414 | 1 R13018 | 1B1 IgG aberrant 1 |
| 6 | 513.5 | 83.5 | 414 | 1 R13111 | 1B1 IgG aberrant 1 |
| 7 | 509.5 | 82.8 | 214 | 1 Y06842 | Seq ID No:10 of JP |
| 8 | 504.5 | 82.0 | 134 | 1 W11155 | Anti-lung tumour a |
| 9 | 499 | 81.1 | 129 | 1 R41286 | F105 rearranged va |
| 10 | 497 | 80.8 | 129 | 1 R38673 | F105VK-F105JK. DNA |
| 11 | 484 | 80.3 | 150 | 1 W40069 | Human monoclonal a |
| 12 | 493.5 | 80.2 | 401 | 1 R12129 | ORF 1 of IgE light |
| 13 | 490.5 | 79.8 | 127 | 1 W08946 | Kappa light chain |
| 14 | 489 | 79.5 | 115 | 1 R38648 | Human V-kappa vk65 |
| 15 | 489 | 79.5 | 115 | 1 R62928 | Human V-kappa vk65 |
| 16 | 489 | 79.5 | 115 | 1 W41144 | Human vkappa65.3 f |
| 17 | 489 | 79.5 | 115 | 1 W62182 | Human DNA vkappa65 |
| 18 | 480 | 78.0 | 124 | 1 W24539 | Immunoglobulin T10 |
| 19 | 476.5 | 77.5 | 120 | 1 W03946 | DNA fragment vk65. |
| 20 | 475.5 | 77.3 | 127 | 1 R50192 | Light chain variab |
| 21 | 474.5 | 77.2 | 109 | 1 W84045 | Human ab light cha |
| 22 | 474 | 77.1 | 110 | 1 W27546 | Human ab light cha |
| 23 | 469.5 | 76.3 | 127 | 1 R50187 | Light chain variab |
| 24 | 469.5 | 76.3 | 128 | 1 P91001 | Anti-P. aeruginosa |
| 25 | 466.5 | 75.9 | 127 | 1 R50191 | Light chain variab |
| 26 | 465 | 75.6 | 115 | 1 R38649 | Human V-kappa frag |
| 27 | 465 | 75.6 | 115 | 1 R62929 | Human V-kappa vk65 |
| 28 | 465 | 75.6 | 115 | 1 W03947 | DNA fragment vk65. |
| 29 | 465 | 75.6 | 115 | 1 W41145 | Human vkappa65.5 f |
| 30 | 465 | 75.6 | 115 | 1 W62183 | Human DNA vkappa65 |
| 31 | 463.5 | 75.4 | 116 | 1 R38650 | Human V-kappa frag |
| 32 | 463.5 | 75.4 | 116 | 1 R62930 | Human V-kappa vk65 |
| 33 | 463.5 | 75.4 | 116 | 1 W03948 | DNA fragment vk65. |

| | | | | | |
|----|-------|------|-----|----------|--------------------|
| 34 | 463.5 | 75.4 | 116 | 1 W41146 | Human vkappa65.8 f |
| 35 | 463.5 | 75.4 | 116 | 1 W62184 | Human DNA vkappa65 |
| 36 | 458 | 74.5 | 107 | 1 R54308 | Anti-HIV gp120 imm |
| 37 | 458 | 74.5 | 107 | 1 W01266 | VL region of HIV n |
| 38 | 457.5 | 74.4 | 105 | 1 W31725 | Alpha light chain |
| 39 | 453.5 | 73.7 | 107 | 1 R38593 | Human lambda light |
| 40 | 453.5 | 73.7 | 107 | 1 W58493 | Human kappa light |
| 41 | 453.5 | 73.7 | 109 | 1 R50218 | HSV glycoprotein F |
| 42 | 453.5 | 73.7 | 238 | 1 W83034 | Anti-Fas humanised |
| 43 | 452 | 73.5 | 287 | 1 W40071 | Human H11-scFv con |
| 44 | 452 | 73.5 | 304 | 1 W40070 | Human H11-scFv con |
| 45 | 449 | 73.0 | 108 | 1 R54316 | Anti-HIV gp120 imm |

ALIGNMENTS

| | |
|---------------------------|---|
| RESULT 1 | |
| R52951 | R52951 standard; Protein; 234 AA. |
| AC | R52951: |
| DT | 27-OCT-1994 (first entry) |
| DE | Human anti-IgE MAb light chain. |
| KM | Human IgE; CH4 region; triggers mediator release; |
| KW | Mast cells; Monoclonal antibody; allergy. |
| OS | Homo sapiens. |
| FH | Key |
| FT | Location/Qualifiers |
| FT | region 21..128 |
| PN | EP-592230-A. |
| PD | 13-APR-1994. |
| PF | 07-OCT-1993; 308006. |
| PR | 07-OCT-1993; JP-293800. |
| PA | (SNOW) SNOW BRAND MILK PROD CO LTD. |
| PI | Goto M, Kobayashi F, Mizuno A, Morinaga T, Washida N; |
| PI | Yoshida T; |
| DR | WPI; 94-120330/15. |
| DR | N-PSDB: 071872. |
| PT | Human monoclonal anti-IgE peptide antibody - inhibits histamine |
| PT | release from mast cells by allergen stimulation, useful for |
| PT | preventing allergies |
| PS | Claim 3; Page 12; 21pp; English. |
| CC | R52951 shows the light chain of a human type anti-IgE peptide |
| CC | monoclonal antibody which inhibits the signal transmission for |
| CC | the release of chemical mediator from mast cells and basophils |
| CC | stimulated with allergen. The antibody can be used for the |
| CC | propylaxis and the therapy of allergy. |
| SC | Sequence 234 AA; |
| Query Match | 87.6%; Score 538.5; DB 1; Length 234; |
| Best Local Similarity | 87.9%; Pred. No. 2.5e-33; |
| Matches 102; Conservative | 9; Mismatches 4; Indels 1; Gaps 1; |
| OY | 1 LMLPDTTGEIVMTQSPATLSVSPGERATLSCRASQSVSSNLAAYQOKPGQAPRLTYGAS 60 |
| DB | 13 LMLPDTTGEIVMTQSPATLSVSPGERATLSCRASQSVSSNLAAYQOKPGQAPRLTYGAS 72 |
| OY | 61 TRATGIPARSSGSGSGLTEFLTITSSLSQSEDFAYVYCOQYNNMPRYTFGQTKLEIKR 116 |
| DB | 73 TRATGIPARSSGSGSGLTEFLTITSSLSQSEDFAYVYCOQYNSM-PRTFGQTKYDLK 127 |
| RESULT 2 | |
| R38672 | R38672 standard; Protein; 129 AA. |
| ID | R38672: |
| AC | 01-NOV-1993 (first entry) |
| DT | 01-NOV-1993 |
| DE | VK325-Jk2. |
| KM | Monoclonal antibody; MAb; envelope; glycoprotein; gp120; HIV; AIDS; |
| KW | CD4; receptor; hydridoma; polymerase chain reaction; PCR; heavy; light; |
| KW | chain; epitope; immune deficiency. |
| OS | Homo sapiens. |

| | | |
|--------|--|---|
| FH | Key | Location/Qualifiers |
| FT | peptide | 1..20 |
| FT | protein | /label= sig_peptide |
| FT | region | 21..129 |
| FT | region | /label= mat_protein |
| FT | region | 1..116 |
| FT | region | /label= VK325 |
| FT | region | 117..129 |
| FT | region | /label= Jk2 |
| FT | region | 44..55 |
| FT | region | /label= CDRI |
| FT | region | 71..77 |
| FT | region | /label= CDR2 |
| FT | region | 110..117 |
| FT | misc_difference | /label= CDR3 |
| FT | misc_difference | 1 |
| FT | misc_difference | /note= "Met encoded by ATC (sic)" |
| FT | misc_difference | 35 |
| FT | misc_difference | /note= "Pro encoded by GCA (sic)" |
| FT | misc_difference | 99 |
| FT | misc_difference | /note= "Leu encoded by GTG (sic)" |
| FT | misc_difference | 113 |
| FT | misc_difference | /note= "Gly encoded by GAT (sic)" |
| FT | misc_difference | 114 |
| FT | misc_difference | /note= "Ser encoded by AAC (sic)" |
| FT | misc_difference | 116 |
| FT | misc_difference | /note= "Pro encoded by GTT (sic)" |
| PN | WO9312232-A. | |
| PD | 24-JUN-1993. | |
| PF | 10-DEC-1992. | U10928. |
| PR | 10-DEC-1991; | US-804652. |
| PA | (DAND) DNA FARMER CANCER INST INC. | |
| PI | (NEW) NEW ENGLAND DEACONNESS HOSPITAL CORP. | |
| PI | Haskelline WA, Marasco WA, Posner MR, Sodroski JG; | |
| DR | WPI; 93-214174/26. | |
| DR | N-PSDB; 042706. | |
| PT | DNA segments encoding monoclonal antibody - which binds to gp120 | |
| PT | and neutralises HIV, for treating AIDS, and for diagnosing and | |
| PT | monitoring HIV infection | |
| PL | Disclosure: Page 74-75; 109pp; English. | |
| CC | The nucleotide sequence of F105 VK (042707 - sequence differs from | |
| CC | other F105 VK sequences given elsewhere in the specification) was | |
| CC | compared with gemline gene HumvK325 (042706), showing 97.7% | |
| CC | similarity. By nucleotide sequence analysis, F105 appears to | |
| CC | be derived from a member of the VK III subgroup gene family. | |
| SO | Sequence 129 AA: | |
| ● | Best Local Similarity | 85.0%; Score 523; DB 1; Length 129; |
| ● | Matches 103; Conservative | 87.3%; Pred. No. 2e-33; 7; Mismatches 6; Indels 2; Gaps |
| OY | 1 LMLPTTGELIYWQTGPAILSVSPGERATISCRASOSVSSN-LAWYOQKGAPRLITYGA | 59 |
| b | 13 LMLPTTGELIYWQTGPAILSVSPGERATISCRASOSVSSYLAWYOQKGAPRLITYGA | 72 |
| OY | 60 STRATGIPARESGSGTEFLTISLSOEDRAVVYYCCOQNNMPPTFGQRTLEIKR | 117 |
| Db | 73 SSRATGIPDRFSGSGSDEFTLTISLREPEDRAVVYYCCOQYG-SPTFGQRTLEIKR | 129 |
| RESULT | 3 | |
| ID | W47582 | |
| AC | W47582 standard; Protein; 117 AA. | |
| DT | 22-JUN-1998 (first entry) | |
| DE | Human monoclonal antibody light chain variable region. | |
| KM | Human; monoclonal antibody; hybridoma cell strain Tt6c; hMAb; | |
| KW | antitetanus toxin. | |
| OS | Homo sapiens. | |
| FT | Key | Location/Qualifiers |
| FT | Region | 24..34 |
| FT | | /label= CDRI |

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FT      Region              49..55
FT      /label= CDR2
FT      Region              89..98
FT      /label= CDR3
PD      JI0014570-A.
PD      20-JAN-1998.
PF      05-JUL-1996; 194095.
PR      05-JUL-1996; JP-194095.
PA      (MATS/) MATSUDA M.
PA      (MOMI) MORINAGA & CO LTD.
PI      WPI: 98-138233/13.
DR      N-PSDB; V18674.
PT      New cDNA encoding human monoclonal antibody - useful for production
PT      of antibody by hybridoma techniques commercially
PS      Claim 4; Fig 2; 8pp; Japanese.
CC      The present sequence represents a human monoclonal antibody (hmab)
CC      light chain variable region. The cDNA encoding the hmab can be used
CC      for commercial production of the hmab. The cDNA was isolated from an
CC      antitelanus toxin human monoclonal antibody producing hybridoma cell
CC      strain VTG6.
SQ      Sequence 117 AA;

Query Match          84.2%; Score 518; DB 1; Length 117;
Best Local Similarity 90.8%; Pred. No. 4.3e-32;
Matches 99; Conservatly 6; Mismatches 2; Indels 0; Gaps 0;

OY      9 EIVMTQSPATISVSNGERTLSCSRASQSVSSNLAWYQKPGAPRLITYGASTRATGIPA 68
Db      1 DIVMTQSPATISVSGENRTLSCSRASQSVGTILAWYQKPGAPRLITYGASTRATGINA 60
        |||.....|||.....|.....|.....|.....|.....|.....|.....|.....|
OY      69 RFSSGGSTEEFLTRITSSLOSEDFAVYYCOQNNMPYPTEFGQTKLEIKR 117
Db      61 RFSGGSGTEFLTRITSSLOSEDFAVYYCOQNSDMPPEPQEGGTKEIR 109
        |||.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|

RESULT   4
R12128
ID       R12128 standard; Protein; 349 AA.
AC       R12128;
DE       01-AUG-1991 (first entry)
DT       1B1 IgG aberrant light chain with duplicated variable region.
KW       Immunoglobulin G; light chain; variable region; duplication.
KV       passive immunity; group B streptococci.
OS       Homo sapiens.
FH       Key
FT       Location/Qualifiers
FT       peptide
           1..117
FT       /label= leader peptide
           18..130
FT       /label= variable region
           /note= "L/V 1"
FT       region
           131..243
FT       /label= variable region
           /note= "L/V 2"
FT       region
           244..345
FT       /label= constant region

FN       WO9106305-A.
PN       16-MAY-1991.
PF       06-NOV-1990; U06426.
PR       07-NOV-1989; US-432700.
PA       (BRIM ) BRISTOL-MYERS SQUIB.
PI       Shuford MW, Harris LJ, Ratf HV;
DR       WPI: 91-163947/22.
DR       N-PSDB; Q11878.
PT       Oligonucleic immunoglobulin(s) with high avidity for antigen(s) -
PT       formed by duplicating esp. variable region of light chain of igg
PT       class .
PS      Example 5; fig 16; 104pp; English.
CC      This sequence is deduced from the cDNA clone 4B9-Vk15 and includes
CC      the amino acid sequence beyond the first stop codon. The clone is
CC      incomplete, starting from the G of the ATG initiator codon, but the
CC      initial Met is given. Antibody molecules of the invention can
CC      include one or two aberrant light chains containing a duplicated

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CC variable region, to produce heavier antibodies. These heavier
 CC antibodies were found to have higher avidity than antibodies with
 CC just a single copy of the L/V region. The antibodies can be used to
 CC treat disease, e.g. infection by Streptococcus agalactiae. They are
 CC able to pass across the placenta.
 CC See also Q11879 and Q11880.
 SQ Sequence 349 AA;

Query Match 83.5%; Score 513.5; DB 1; Length 349;
 Best Local Similarity 85.5%; Pred. No. 2,6e-31;
 Matches 100; Conservative 6; Mismatches 10; Indels 1; Gaps 1;

OY 1 LWPDTGEIVMTQSPATLSVSPGERATLSCRASSQSVSNLAWYQOKPGQAPRLIYGAS 60
 DB 13 LWPDTGEIVLQSPATLSLSPGERATLSCRASSQSVGYLAWYQOKPGQAPRLIYDAS 72
 OY 61 TRATGIPARFSGSGSTEFTLTISLQSEDFAVYYCCQYNNMPP-YTFGCGTRLEIK 116
 D 73 NRATGIPARFSGSGSTEFTLTISLQSEDFAVYYCQHRDNMPGATFGGTRKVEIK 129

RESULT 5
 R13018
 ID R13018 standard; Protein: 414 AA.

AC R13018:
 DT 01-AUG-1991 (first entry)
 DE 1B1 IgG aberrant light chain with duplicated variable region.
 KW Immunoglobulin G; light chain; variable region; duplication;
 KW passive immunity; group B streptococci.
 OS Homo sapiens.

FT Key Location/Qualifiers
 FT peptide 1..17
 FT /label= leader peptide
 FT region 18..130
 FT /label= variable region
 FT /note= "L/V 1"
 FT region 131..243
 FT /label= variable region
 FT /note= "L/V 2"
 FT region 244..345
 FT /label= constant region

PD WO9106305-A.
 PD 16-MAY-1991. U06426.
 PR 06-NOV-1990; U06426.
 PR 07-NOV-1989; US-432700.
 PI (BRIM) BRISTOL-MYERS SQUIB.
 PI Shuford MW, Harris LJ, Raff HV;
 PI MPI: 91-163947/22.
 DR N-PEDB; Q11878.

PT Oligomeric Immunoglobulin(s) with high avidity for antigen(s) -
 PT formed by duplicating esp. variable region of light chain of IgG
 PT Class

PS Example 5; Fig 16; 104pp; English.
 CC This sequence is deduced from the cDNA clone 489-VK15 and includes
 CC the amino acid sequence beyond the first stop codon ("x" in the
 CC sequence represents a nonsense codon). The clone is incomplete,
 CC starting from the G of the ATG initiator codon, but the initial Met
 CC is given. Antibody molecules of the invention can include one or two
 CC aberrant light chains containing a duplicated variable region, to
 CC produce heavier antibodies. These heavier antibodies were found to
 CC have higher avidity than antibodies with just a single copy of the
 CC L/V region. The antibodies can be used to treat disease, e.g.
 CC infection by Streptococcus agalactiae. They are able to pass across
 CC the placenta.
 CC See also Q11879 and Q11880.

SQ Sequence 414 AA;

Query Match 83.5%; Score 513.5; DB 1; Length 414;
 Best Local Similarity 85.5%; Pred. No. 3e-31;
 Matches 100; Conservative 6; Mismatches 10; Indels 1; Gaps 1;

OY 1 LWPDTGEIVMTQSPATLSVSPGERATLSCRASSQSVSNLAWYQOKPGQAPRLIYGAS 60
 DB 13 LWPDTGEIVLQSPATLSLSPGERATLSCRASSQSVGYLAWYQOKPGQAPRLIYDAS 72
 OY 61 TRATGIPARFSGSGSTEFTLTISLQSEDFAVYYCCQYNNMPP-YTFGCGTRLEIK 116
 DB 73 NRATGIPARFSGSGSTEFTLTISLQSEDFAVYYCQHRDNMPGATFGGTRKVEIK 129

RESULT 6
 R13111
 ID R13111 standard; Protein: 414 AA.

AC R13111:
 DT 10-MAR-1993 (revised)
 DT 01-AUG-1991 (first entry)
 DE 1B1 IgG aberrant light chain with duplicated variable region.
 KW Immunoglobulin G; light chain; variable region; duplication;
 KW passive immunity; group B streptococci.
 OS Homo sapiens.

FT Key Location/Qualifiers
 FT peptide 1..17
 FT /label= leader peptide
 FT region 18..130
 FT /label= variable region
 FT /note= "L/V 1"
 FT region 131..243
 FT /label= variable region
 FT /note= "L/V 2"
 FT region 244..345
 FT /label= constant region

PD WO9106305-A.
 PD 16-MAY-1991. U06426.
 PR 06-NOV-1990; U06426.
 PR 07-NOV-1989; US-432700.
 PI (BRIM) BRISTOL-MYERS SQUIB.
 PI Shuford MW, Harris LJ, Raff HV;
 PI MPI: 91-163947/22.
 DR N-PEDB; Q11878.

PT Oligomeric Immunoglobulin(s) with high avidity for antigen(s) -
 PT formed by duplicating esp. variable region of light chain of IgG
 PT Class

PS Example 5; Fig 16; 104pp; English.
 CC This sequence is deduced from the cDNA clone 489-VK15 and includes
 CC the amino acid sequence beyond the first stop codon ("x" in the
 CC sequence represents a nonsense codon). The clone is incomplete,
 CC starting from the G of the ATG initiator codon, but the initial Met
 CC is given. Antibody molecules of the invention can include one or two
 CC aberrant light chains containing a duplicated variable region, to
 CC produce heavier antibodies. These heavier antibodies were found to
 CC have higher avidity than antibodies with just a single copy of the
 CC L/V region. The antibodies can be used to treat disease, e.g.
 CC infection by Streptococcus agalactiae. They are able to pass across
 CC the placenta.
 CC See also Q11879 and Q11880.

SQ Sequence 414 AA;

Query Match 83.5%; Score 513.5; DB 1; Length 414;
 Best Local Similarity 85.5%; Pred. No. 3e-31;
 Matches 100; Conservative 6; Mismatches 10; Indels 1; Gaps 1;

OY 1 LWPDTGEIVMTQSPATLSVSPGERATLSCRASSQSVSNLAWYQOKPGQAPRLIYGAS 60
 DB 13 LWPDTGEIVLQSPATLSLSPGERATLSCRASSQSVGYLAWYQOKPGQAPRLIYDAS 72
 OY 61 TRATGIPARFSGSGSTEFTLTISLQSEDFAVYYCCQYNNMPP-YTFGCGTRLEIK 116
 DB 73 NRATGIPARFSGSGSTEFTLTISLQSEDFAVYYCQHRDNMPGATFGGTRKVEIK 129

RESULT 7
 Y06842
 ID Y06842 standard; Protein: 214 AA.

AC Y06842; (first entry)
DT 25-JUN-1999
Seq ID No.10 of JP1089576.
KW AntiHbs: monoclonal antibody; Epstein Barr virus; EBV; adr type:
KM human; Hbs antigen; hepatitis C.
OS Homo sapiens.
PN J11089576-A.
PD 06-APR-1999.
PF 19-SEP-1997: 255705.
PA 19-SEP-1997: JP-255705.
RA (NISN) NISSHINO IND INC.
DR WPI: 99-281053/24.
DR N-PSDB: X32826.
PT Anti-Hbs monoclonal antibody - produced without the risk of Epstein
PT Barr virus contamination
PS Disclosure: Page 9-10; 12pp; Japanese.
CC The invention relates to an antiHbs monoclonal antibody having the
CC following properties: (A) CDR-3 of H chain variable region; (B) it
CC contains no Epstein Barr virus (EBV); (C) it binds at least one adr type
CC among human Hbs antigens. The antiHbs monoclonal antibody is high in
CC antibody titer and has low risk of EBV contamination. It can be used to
CC prevent hepatitis C.
SQ Sequence 214 AA;

Query Match 82.8%; Score 509.5; DB 1; Length 214;
Best Local Similarity 93.6%; Pred. No. 3.2e-31;
Matches 102; Conservative 1; Mismatches 5; Indels 1; Gaps 1;
DY 9 EIVMTQSPATISVSPGERATLSCRASQSVSSNLTANYQKPGAPRLIYGASTRATGIPA 68
DB 1 EIVMTQSPATISVSPGERATLSCRASQSVSSNLTANYQKPGAPRLIYGASTRATGIPA 60
DY 69 RFSGSGSTFEFTLTISLSQSEDFAVYCCQYNNMPPTFGGCKLEIKR 117
DB 61 RFSGSGSTFEFTLTISLSQSEDFAVYCCQYNNMPPTFGGCKLEIKR 108

RESULT 8
W11155
ID W11155 standard; Protein; 134 AA.
AC W11155;
DT 14-MAY-1997 (first entry)
DE Anti-lung tumour antigen monoclonal antibody light chain.
KW Light chain monoclonal; antibody; TB2A36C3; lung; tumour; EBV;
KM Epstein-Barr virus; TB945; human; B cell; screen; antigen;
KW Carcinoma; lysis; anti-tumour therapy; activation; CD4; CD8;
KM B-cell.
OS Homo sapiens.
PN WO9628473-A1.
PD 19-SEP-1996.
PF 18-MAR-1996: U03661.
PA 16-MAR-1995: US-405034.
RA (MEDA) MEDENICA R D.
PI Mukerjee S; 4/3.
DR WPI: 96-433764/43.
DR N-PSDB: T33664.
PT Anti-lung tumour antigen monoclonal antibody TB2A36C3 - produced by
PT Epstein-Barr virus transformation of human lung cancer patient
PT B-cells, useful in conjunction with other agents for lysis of
PT tumours
PS Claim 12; Page 25; 46pp; English.
CC The present sequence is the light chain from the monoclonal
CC antibody (Mab) TB2A36C3, which has high specificity against lung
CC tumour antigens and is produced by an Epstein-Barr virus (EBV)
CC transformed TB945 human B cell line. The Mab can be used to screen
CC serum or tissue samples for a carcinoma associated antigen, lyse
CC tumours in anti-tumour therapy (optionally with other agents) and
CC activate immune competent CD4 or CD8 cells in a patient's blood
CC system.
CC Tumour draining lymph nodes obtained from a non-SCLC (small cell
CC lung cancer) patient were cut into fine pieces and mashed. Pure B
CC cells, isolated using CD19 coated immunomagnetic beads, were

CC immortalised by EBV transformation, and plated and assayed for
CC activity. Clones which showed positive reactivity with autologous
CC tumour cells from the patient and the SCLC cell line NC1H69, were
CC subjected to limiting dilution to prepare the Mab.
SQ Sequence 134 AA;

Query Match 82.0%; Score 504.5; DB 1; Length 134;
Best Local Similarity 84.7%; Pred. No. 4.8e-31;
Matches 100; Conservative 5; Mismatches 12; Indels 1; Gaps 1;

DY 1 LMLPDTGEIYMTQSPATISVSPGERATLSCRASQSVSSNLTANYQKPGAPRLIYGA 59
DB 13 LMLPDTGEIYMTQSPATISVSPGERATLSCRASQSVSSNLTANYQKPGAPRLIYGA 72
DY 60 STRATGIPARFSGSGSTFEFTLTISLSQSEDFAVYCCQYNNMPPTFGGCKLEIKR 117
DB 73 STRATGIPARFSGSGSTFEFTLTISLSQSEDFAVYCCQYNNMPPTFGGCKLEIKR 130

RESULT 9
R41286
ID R41286 standard; Protein; 129 AA.
AC R41286;
DT 01-NOV-1993 (first entry)
DE F105 rearranged variable region light chain.
KW Monoclonal antibody; Mab; envelope; glycoprotein; gp120; HIV; AIDS;
KW CD4; receptor; hybridoma; polymerase chain reaction; PCR; heavy; light;
KW chain; epitope; immune deficiency.
OS Homo sapiens.
FH Key Location/Qualifiers
FT peptide 1..19
FT protein 20..129
FT /label= sig_peptide
FT /label= mat_protein
PN WO9312232-A.
PD 24-JUN-1993.
PF 10-DEC-1992: U10928.
PA 10-DEC-1991: US-804652.
RA (DAND) DANA FARBER CANCER INST INC.
PA (NEW) NEW ENGLAND DECONNESS HOSPITAL CORP.
PI Haseltine WA, Marasco WA, Posner MR, Sodroski JG;
DR WPI: 93-214174/26.
DR N-PSDB: Q49155.
PT DNA segments encoding monoclonal antibody - which binds to gp120
PT and neutralises HIV, for treating AIDS, and for diagnosing and
PT monitoring HIV infection
PS Claim 10; Page 79; 109pp; English.
CC mRNA from the known hybridoma F105 was converted to cDNA and this
CC subjected to PCR amplification using primers corresp. to appropriate
CC parts of the heavy or light chains and having restriction sites to
CC permit cloning. The extension prods. were isolated and sequenced.
CC The recombinant human monoclonal antibody (Mab) binds to a
CC discontinuous epitope on the HIV gp120 envelope glycoprotein, blocks
CC the binding of gp120 to the CD4 receptor, and neutralises a broad
CC range of HIV isolates. The Mab may be used to treat immune
CC deficiency, esp. at doses of 0.1-10 mg/kg.
SQ Sequence 129 AA;

Query Match 81.1%; Score 499; DB 1; Length 129;
Best Local Similarity 84.7%; Pred. No. 1.2e-30;
Matches 100; Conservative 7; Mismatches 9; Indels 2; Gaps 2;

DY 1 LMLPDTGEIYMTQSPATISVSPGERATLSCRASQSVSSNLTANYQKPGAPRLIYGA 59
DB 13 LMLPDTGEIYMTQSPATISVSPGERATLSCRASQSVSSNLTANYQKPGAPRLIYGA 72
DY 60 STRATGIPARFSGSGSTFEFTLTISLSQSEDFAVYCCQYNNMPPTFGGCKLEIKR 117
DB 73 STRATGIPARFSGSGSTFEFTLTISLSQSEDFAVYCCQYNNMPPTFGGCKLEIKR 129

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RESULT 10
ID R38673
AC R38673 standard; Protein: 129 AA.
DT 01-NOV-1993 (first entry)
DE F105K-F105JK.
KW Monoclonal antibody; Mab; envelope; glycoprotein; gp120; HIV; AIDS;
KW CD4; receptor; hydridoma; polymerase chain reaction; PCR; heavy; light;
KW chain; epitope; immune deficiency.
OS Homo sapiens.
FH Key
FT Location/Qualifiers
FT 1..20
FT /label= sig_peptide
FT 21..129
FT /label= mat_protein
FT 1..116
FT /label= F105VK
FT 117..129
FT /label= F105JK
FT 44..55
FT /label= CDR1
FT 71..77
FT /label= CDR2
FT 110..117
FT /label= CDR3
FT misc_difference 1
FT /note= "Met encoded by ATC (sic)"
FT misc_difference 35
FT /note= "Pro encoded by GCA (sic)"
FT misc_difference 99
FT /note= "Leu encoded by GTG (sic)"
FT misc_difference 113
FT /note= "Gly encoded by GAR (sic)"
FT misc_difference 114
FT /note= "Ser encoded by AAC (sic)"
FT misc_difference 116
FT /note= "Pro encoded by GTT (sic)"
FT WO9312232-A.
FT 24-JUN-1993.
FT 10-DEC-1992: U10928.
FT 10-DEC-1991: US-804652.
FT (DAND ) DANA FARBER CANCER INST INC.
FT (NEW-) NEW ENGLAND DEACONNESS HOSPITAL CORP.
FT Haseltine WA, Marasco WA, Posner MR, Sodroski JG;
FT WPI: 93-214174/26.
FT N-PSDB; Q42706.
FT DNA segments encoding monoclonal antibody - which binds to gp120
FT and neutralises HIV, for treating AIDS, and for diagnosing and
FT monitoring HIV infection
FT Disclosure: Page 74-75: 1099P; English.
FT The nucleotide sequence of F105 VK (Q42707 - sequence differs from
FT other F105 VK sequences given elsewhere in the specification) was
FT compared with germline gene HumvK325 (Q42706), showing 97.7%
FT similarity. By nucleotide sequence analysis, F105 appears to
FT be derived from a member of the VK III subgroup gene family.
FT Sequence 129 AA.

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Query Match 80.8%; Score 497; DB 1; Length 129;
 Best Local Similarity 84.7%; Pred. No. 1.7e-30;
 Matches 100; Conservative 7; Mismatches 9; Indels 2; Gaps 2;

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QY 1 LMPDPTGELVMTQSPATLSVSPGERATLSCRSQSVSN-SNLAWYQKQPGQARLLIYGA 59
DB 13 LMPDPTGELVMTQSPATLSVSPGERATLSCRSQSVSN-SNLAWYQKQPGQARLLIYGA 72
QY 60 STRATGIPARFSGSGGTEFTLTISLSQSEDFAVYYCOQNNMPYFGGQTKLEIKR 117
DB 73 SSRATGIPARFSGSGGTEFTLTISLSQSEDFAVYYCOQIDN-SVCTFGGQTKLEIKR 129

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ID W40069;
AC W40069 standard; Protein: 150 AA.
DT 29-MAY-1998 (first entry)
DE Human monoclonal antibody H11 protein variable region H chain.
KW H11; monoclonal antibody; Mab; C-antigen; variable region heavy chain;
KW V region; H chain; neoplasia; detection; lymphoma; tumour cell; probe;
KW primer; vaccine; gene therapy; glioblastoma; neuroblastoma;
KW malignant melanoma; adenocarcinoma; small cell lung carcinoma.
OS Homo sapiens.
FH Key
FT Location/Qualifiers
FT 1..20
FT /label= sig_peptide
FT 21..129
FT /label= mat_protein
FT 1..116
FT /label= F105VK
FT 117..129
FT /label= F105JK
FT 44..55
FT /label= CDR1
FT 71..77
FT /label= CDR2
FT 110..117
FT /label= CDR3
FT misc_difference 1
FT /note= "Met encoded by ATC (sic)"
FT misc_difference 35
FT /note= "Pro encoded by GCA (sic)"
FT misc_difference 99
FT /note= "Leu encoded by GTG (sic)"
FT misc_difference 113
FT /note= "Gly encoded by GAR (sic)"
FT misc_difference 114
FT /note= "Ser encoded by AAC (sic)"
FT misc_difference 116
FT /note= "Pro encoded by GTT (sic)"
FT WO9312232-A.
FT 24-JUN-1993.
FT 10-DEC-1992: U10928.
FT 10-DEC-1991: US-804652.
FT (DAND ) DANA FARBER CANCER INST INC.
FT (NEW-) NEW ENGLAND DEACONNESS HOSPITAL CORP.
FT Haseltine WA, Marasco WA, Posner MR, Sodroski JG;
FT WPI: 93-214174/26.
FT N-PSDB; Q42706.
FT DNA segments encoding monoclonal antibody - which binds to gp120
FT and neutralises HIV, for treating AIDS, and for diagnosing and
FT monitoring HIV infection
FT Disclosure: Page 74-75: 1099P; English.
FT The nucleotide sequence of F105 VK (Q42707 - sequence differs from
FT other F105 VK sequences given elsewhere in the specification) was
FT compared with germline gene HumvK325 (Q42706), showing 97.7%
FT similarity. By nucleotide sequence analysis, F105 appears to
FT be derived from a member of the VK III subgroup gene family.
FT Sequence 129 AA.

```

Query Match 80.3%; Score 494; DB 1; Length 150;
 Best Local Similarity 81.0%; Pred. No. 3.2e-30;
 Matches 98; Conservative 9; Mismatches 10; Indels 4; Gaps 2;

```

QY 1 LMPDPTGELVMTQSPATLSVSPGERATLSCRSQSVSN-SNLAWYQKQPGQARLLIYGA 59
DB 17 LMPDPTGELVMTQSPATLSVSPGERATLSCRSQSVSN-SNLAWYQKQPGQARLLIYGA 76
QY 60 STRATGIPARFSGSGGTEFTLTISLSQSEDFAVYYCOQNNMPYFGGQTKLEIKR 116
DB 77 STRATGIPARFSGSGGTEFTLTISLSQSEDFAVYYCOQNNMPYFGGQTKLEIKR 136
QY 117 R 117
DB 137 R 137

```

DR WPI: 91-163947/22.
 DR N-PSDB: Q11879.
 PT Oligomeric immunoglobulin(s) with high avidity for antigen(s) -
 PT formed by duplicating esp. variable region of light chain of IgG
 PT class
 PS Example 4; Fig 17; 104pp; English.
 CC This sequence is derived from the nucleotide sequence encoding the
 CC light chain variable region. The "x" residues represent nonsense
 CC codons. The coding sequence has been translated in all 3 reading
 CC frames (see also R12130 and R12131). The L/V region is duplicated
 CC in so-called "aberrant" light chains (see Q11878), conferring
 CC increased avidity on antibodies comprising such aberrant chains.
 CC See also Q11880.
 SQ Sequence 401 AA;

Query Match 80.2%; Score 493.5; DB 1; Length 401;
 Best Local Similarity 83.6%; Pred. No. 8.8e-30;

Matches 97; Conservative 7; Mismatches 11; Indels 1; Gaps 1;

OY 3 LPTDTGEIYVWTSPTATLSVSPGERATLSCRASQSVSNLAWYQKPGAPRLIIGASTR 62
 : |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
 DB 221 IDDTGEIYVWTSPTATLSVSPGERATLSCRASQSVSNLAWYQKPGAPRLIIGASTR 280
 OY 63 ATGIPARFSGSGGTFTLTLSLSEDFAVYVYCCQYNNMPP-YTGGCTKLEIKR 117
 : |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
 DB 281 ATGIPARFSGSGGTFTLTLSLSEDFAVYVYCCQYNNMPP-YTGGCTKLEIKR 336

RESULT 13

W08946
 ID W08946 standard; Protein: 127 AA.

AC W08946;
 DT 18-SEP-1997 (first entry)
 DE Kappa light chain variable region of 225RA antibody.
 KM Kappa; light chain; reshaped; monoclonal; antibody; 225RA;
 KM human; epidermal growth factor; EGF; receptor; inhibition; growth;
 KM tumour; cell; late stage; prostatic; prostate; variable region.
 OS Homo sapiens.
 PN W09640210-A1.
 PD 19-DEC-1996.
 PF 07-JUN-1996; U09847.
 PR 07-JUN-1995; US-482982.
 PR 15-DEC-1995; US-573289.
 PA (IMCL-) IMCLONE SYSTEMS INC.
 PA (MRC-) MRC COLLABORATIVE CENT.
 PI Giorgio NA, Goldstein NI, Jones ST, Saldanha JW.
 PI WPI: 97-051897/05.
 DR N-PSDB: T49345.
 PT Chimeric and humanised versions of anti-EGF receptor antibody 225 -
 PT used for inhibiting tumour growth, esp. of late stage prostatic
 PT tumour
 PS Claim 31; Fig 19; 112pp; English.
 CC The present sequence is the kappa light chain variable region
 CC of the reshaped human monoclonal antibody (MAb) H225, 225RA. The
 CC MAb is specific for the human epidermal growth factor (EGF)
 CC receptor.
 CC The MAb, or a fragment, can be used to inhibit the growth of tumour
 CC cells, especially late stage prostatic tumour cells in humans,
 CC optionally conjugated to a cytotoxic agent, especially doxorubicin,
 CC taxol or cisplatin, or a signal transduction, ras or cell cycle
 CC inhibitor.
 SQ Sequence 127 AA;

Query Match 79.8%; Score 430.5; DB 1; Length 127;
 Best Local Similarity 81.0%; Pred. No. 5e-30;

Matches 94; Conservative 10; Mismatches 11; Indels 1; Gaps 1;

OY 1 LMLPTTGEIYVWTSPTATLSVSPGERATLSCRASQSVSNLAWYQKPGAPRLIIGAS 60
 : |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
 DB 13 LMLPTTGEIYVWTSPTATLSVSPGERATLSCRASQSVSNLAWYQKPGAPRLIIGAS 72

OY 61 TRATGIPARFSGSGGTFTLTLSLSEDFAVYVYCCQYNNMPPYTFGGCTKLEIKR 116
 : |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
 DB 73 ESISGIPARFSGSGGTFTLTLSLSEDFAVYVYCCQYNNMPPYTFGGCTKLEIKR 127

RESULT 14

R38648
 ID R38648 standard; Protein: 115 AA.

AC R38648;
 DT 10-NOV-1993 (first entry)
 DE Human V-kappa fragment encoded by clone vk65.3.
 KM Immunoglobulin; light chain variable region; minilocus;
 KM isotype switching; unrearranged functional V κ gene segment;
 KM human light chain transgene.
 OS Homo sapiens.
 PN W09312227-A.
 PD 24-JUN-1993.
 PF 17-DEC-1992; U10983.
 PR 17-DEC-1991; US-810279.
 PR 18-MAR-1992; US-853408.
 PR 23-JUN-1992; US-904068.
 PA (GENP-) GENPHARM INT INC.
 PI Kay RW, Lomberg N.
 PI WPI: 93-214169/26.
 DR N-PSDB: Q44222.
 PT Transgenic non-human animals contg. immunoglobulin heavy chain
 PT trans gene - used to produce useful antibodies by isotype
 PT switching
 PS Example 21; Fig 41; 196pp; English.
 CC The V-kappa specific oligonucleotide Q50327 was used to probe a
 CC human placental genomic DNA library cloned into lambdaEMBL3/SP6/T7.
 CC DNA fragments containing V-kappa segments from positive phage
 CC clones were subcloned into plasmid vectors. Variable gene segments
 CC from the resulting clones were sequenced and functional clones were
 CC selected on the basis of open reading frames, intact donor and
 CC acceptor splice sites and intact recombination sequences. The
 CC sequences obtained from four different plasmid clones were
 CC designated p65.3, p65.5, p65.8 and p65.15 (see Q44222-Q44225,
 CC respectively) and the amino acid sequences of the V-kappa regions
 CC they encode were deduced.
 SQ Sequence 115 AA;

Query Match 79.5%; Score 489; DB 1; Length 115;
 Best Local Similarity 90.3%; Pred. No. 5.8e-30;
 Matches 93; Conservative 5; Mismatches 5; Indels 0; Gaps 0;

OY 1 LMLPTTGEIYVWTSPTATLSVSPGERATLSCRASQSVSNLAWYQKPGAPRLIIGAS 60
 : |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
 DB 13 LMLPTTGEIYVWTSPTATLSVSPGERATLSCRASQSVSNLAWYQKPGAPRLIIGAS 72
 OY 61 TRATGIPARFSGSGGTFTLTLSLSEDFAVYVYCCQYNNMPP 103
 : |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
 DB 73 NRATGIPARFSGSGGTFTLTLSLSEDFAVYVYCCQYNNMPP 115

RESULT 15

R62928
 ID R62928 standard; Protein: 115 AA.

AC R62928;
 DT 07-JUN-1995 (first entry)
 DE Human V-kappa vk65.3 region.
 KM Transgenic mouse; transgenic animal; antibody engineering;
 KM variable region; light chain; minilocus transgene;
 KM chimeric antibody.
 OS Homo sapiens.
 PN W09425585-A.
 PD 10-NOV-1994.
 PF 25-APR-1994; U04580.
 PR 26-APR-1993; US-053131.
 PR 22-JUL-1993; US-096762.
 PR 18-NOV-1993; US-155501.
 PR 03-DEC-1993; US-161739.

PR 10-DEC-1993; US-165699.
 PR 09-MAR-1994; US-209741.
 PA (GENP-) GENPHARM INT INC.
 PI Kay RW, Lomberg N;
 DR N-PSDB; Q7852.
 DR WPI; 94-358263/44.
 PT Transgenic non-human animals producing heterologous or chimeric
 PT antibodies - for binding a pre-determined human antigen with
 PT increased affinity
 PS Disclosure; Fig. 41; 296pp; English.
 CC Human DNA fragments vk65.3, vk65.5, vk65.8 and vk65.15 (given in
 CC Q7852-Q7855, respectively) each contain a V-kappa gene segment
 CC that can be used to form a complete human light chain minilocus
 CC transgene for expression in a nonhuman transgenic animal for
 CC heterologous antibody production. The deduced amino acid
 CC sequences of the V-kappa coding regions are given in R62928-R62931.
 SQ Sequence 115 AA;

Very Match 79.5%; Score 489; DB 1; Length 115;
 St Local Similarity 90.3%; Pred. NO. 5.8e-30;
 Matches 93; Conservative 5; Mismatches 5; Indels 0; Gaps 0;

QY 1 LMLPDTGEIVMTQSPATLSVSPGERATLSCASQSVSNLAWYQKPGAPRLIYGAS 60
 |||||
 DB 13 LMLPDTGEIVLTPSPATLSLSPGERATLSCASQSVSYLAWYQKPGAPRLIYDAS 72
 |||||
 QY 61 TRATGIPARFSGSGGTFTLTISLQSEDFAYVYCOQYNMP 103
 |||||
 DB 73 NRATGIPARFSGSGGTFTLTISLSEDFAYVYCOQRNMP 115
 |||||

Search completed: July 26, 2000, 14:01:27
 Job time: 2766 sec

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GenCore version 4.5
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OM protein - protein search, using sw model

Run on: July 26, 2000, 14:21:22 ; Search time 43.23 seconds
(without alignments)
167.488 Million cell updates/sec

Title: US-09-203-768a-4

Perfect score: 615
Sequence: 1 LMLPDTGELVMTQSPATLS.....QYNNWPPYTFGGTKLEIKR 117

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Search: 178050 seqs, 61884766 residues

Number of hits satisfying chosen parameters: 178050

Minimum DB seq length: 0
Maximum DB seq length: 1000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database: 1: p1r1:*
2: p1r2:*
3: p1r3:*
4: p1r4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match Length | ID | Description |
|------------|-------|--------------------|--------------|--------------------|
| 1 | 588.5 | 95.7 | 128 2 S40343 | Ig kappa chain V-J |
| 2 | 574.5 | 93.4 | 117 2 S40362 | Ig kappa chain - h |
| 3 | 562 | 91.4 | 131 2 S40328 | Ig kappa chain - h |
| 4 | 539.5 | 87.7 | 123 2 S40378 | Ig kappa chain - h |
| 5 | 530.5 | 86.3 | 128 2 A56701 | Ig kappa chain V r |
| 6 | 527 | 85.7 | 115 1 K3HUC1 | Ig kappa chain pre |
| 7 | 526.5 | 85.6 | 107 2 S34005 | Ig kappa chain V r |
| 8 | 526 | 85.5 | 115 2 A30553 | Ig kappa chain pre |
| 9 | 525.5 | 85.4 | 144 2 PLO106 | Ig kappa chain pre |
| 10 | 523 | 85.0 | 116 2 B26555 | Ig kappa chain V-I |
| 11 | 522 | 84.9 | 110 2 S40326 | Ig kappa chain V-J |
| 12 | 518.5 | 84.3 | 128 2 S40379 | Ig kappa chain V-J |
| 13 | 514 | 83.6 | 215 2 JEO244 | Ig kappa chain V r |
| 14 | 513.5 | 83.5 | 129 2 S28627 | Ig kappa chain V r |
| 15 | 511.5 | 83.2 | 114 2 S46375 | Ig kappa chain V r |
| 16 | 510 | 82.9 | 129 1 K3HUA | Ig kappa chain pre |
| 17 | 510 | 82.9 | 129 2 S49532 | anti-Sm antibody V |
| 18 | 510 | 82.9 | 129 2 S46369 | Ig kappa chain V r |
| 19 | 510 | 82.9 | 134 2 S38643 | Ig kappa chain V r |
| 20 | 509.5 | 82.8 | 128 2 S40345 | Ig kappa chain V-J |
| 21 | 509 | 82.8 | 129 1 K3HUI | Ig kappa chain pre |
| 22 | 505 | 82.1 | 108 2 S40377 | Ig kappa chain V-I |
| 23 | 504 | 82.0 | 109 1 K3HUP | Ig kappa chain V-I |
| 24 | 502 | 81.6 | 129 2 A33274 | Ig kappa chain pre |
| 25 | 499 | 81.1 | 128 2 S20636 | Ig kappa chain V r |
| 26 | 498 | 81.0 | 130 2 S20637 | Ig kappa chain V r |
| 27 | 496 | 80.7 | 114 2 S54905 | Ig kappa chain V r |
| 28 | 496 | 80.7 | 130 2 S40360 | Ig kappa chain - h |
| 29 | 494 | 80.3 | 129 2 S40363 | Ig kappa chain - h |

| | | | | |
|----|-------|------|--------------|--------------------|
| 30 | 493.5 | 80.2 | 128 1 K3HUA1 | Ig kappa chain pre |
| 31 | 492.5 | 80.1 | 131 2 S40346 | Ig kappa chain V-J |
| 32 | 490.5 | 79.8 | 111 2 S33628 | Ig kappa chain V r |
| 33 | 489.5 | 79.6 | 125 2 S40344 | Ig kappa chain V-J |
| 34 | 489 | 79.5 | 115 1 K3HUV | Ig kappa chain pre |
| 35 | 485.5 | 78.9 | 129 2 S40325 | Ig kappa chain - h |
| 36 | 485 | 78.9 | 121 2 S40327 | Ig kappa chain - h |
| 37 | 484 | 78.7 | 124 2 S20633 | Ig kappa chain - h |
| 38 | 482.5 | 78.5 | 215 2 JEO243 | Ig kappa chain V r |
| 39 | 479.5 | 78.0 | 119 2 S41816 | Ig kappa chain V r |
| 40 | 478 | 77.7 | 98 2 I30608 | Ig kappa chain V-I |
| 41 | 476 | 77.4 | 95 2 PH0868 | Ig kappa chain V r |
| 42 | 475 | 77.2 | 109 2 H30601 | Ig kappa chain V-I |
| 43 | 471.5 | 76.7 | 108 2 S44151 | Ig kappa chain V r |
| 44 | 467 | 75.9 | 145 2 S20631 | Ig kappa chain - h |
| 45 | 465 | 75.6 | 108 2 C30608 | Ig kappa chain V-I |

ALIGNMENTS

RESULT 1
S40343
Ig kappa chain V-J region - human
C:Species: Homo sapiens (man)
C:Date: 19-May-1994 #sequence_revision 26-May-1995 #text_change 21-Jan-2000
C:Accession: S40343
R:Klein, R.; Jaenichen, R.; Zachau, H.G.
Eur. J. Immunol. 23, 3248-3271, 1993
A:Title: Expressed human immunoglobulin chl genes and their hypermutation.
A:Reference number: S40312; MUID:94080891
A:Accession: S40343
A:Status: preliminary; translation not shown
A:Molecule type: mRNA
A:Residues: 1-128 <KLE>
A:Cross-references: EMBL:X72453; NID:G441374; PIDN:CA51121.1; PID:G441375
C:Superfamily: Immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:36-110/Domain: immunoglobulin homology <IMK>

Query Match 95.7% Score 588.5; DB 2; Length 128;
Best Local Similarity 97.4% Pred. No. 3.8e+42;
Matches 114; Conservative 1; Mismatches 1; Indels 1; Gaps 1;
QY 1 LMLPDTGELVMTQSPATLSVSGERATLSRASQSVSSNLAWYQKRGQAPRLIYGAS 60
DB 13 LMLPDTGELVMTQSPATLSVSGERATLSRASQSVSSNLAWYQKRGQAPRLIYGAS 72
QY 61 TRATGTPARFSSGSGTETFLISSLQSEDFAVYCCQYNNWPPYTFGGTKLEIKR 117
DB 73 TRATGTPARFSSGSGTETFLISSLQSEDFAVYCCQYNNWPPYTFGGTKLEIKR 128
RESULT 2
S40362
Ig kappa chain - human
C:Species: Homo sapiens (man)
C:Date: 06-Mar-1994 #sequence_revision 26-May-1995 #text_change 21-Jan-2000
C:Accession: S40362
R:Klein, R.; Jaenichen, R.; Zachau, H.G.
Eur. J. Immunol. 23, 3248-3271, 1993
A:Title: Expressed human immunoglobulin chl genes and their hypermutation.
A:Reference number: S40312; MUID:94080891
A:Accession: S40362
A:Status: preliminary; translation not shown
A:Molecule type: mRNA
A:Residues: 1-111 <KLE>
A:Cross-references: EMBL:X72472; NID:G441412; PID:G441413
C:Superfamily: Immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:26-100/Domain: immunoglobulin homology <IMK>

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Query Match Similarity      93.4%: Score 574.5; DB 2; Length 117;
Best Local Similarity       96.6%: Pred. No. 4.9e-41;
Matches 112; Conservative   1; Mismatches 2; Indels 1; Gaps 1

OY    1 LMLPDTGTGIWVTOSPATLTVSPGERATLTSCRASQSVSSNLAWYOOKPGQAPRLLITYGAS 60
DB    3 LMLPTTGTGIWVTOSPATLTVSPGERATLTSCRASQSVSSNLAWYOOKPGQAPRLLITYGAS 62

OY    61 TRATGTPARFSGSGSGETFTLTITSSLOSDEFAVYYCOQYNMPPYFGGTLEIKR 116
DB    63 TRATGTPARFSGSGSGETFTLTITSSLOSDEFAVYYCOQYNM-PLTFGGGTVEIKR 117

RESULT      3
SA40328
IG kappa chain - human
C:Species: Homo sapiens (man)
Date: 06-Mar-1994 #sequence_revision 26-May-1995 #text_change 21-Jan-2000
Accession: S40328
R:Klein, R.; Jaenichen, R.; Zachau, H.G.
Eur. J. Immunol. 23, 3248-3271, 1993
A>Title: Expressed human immunoglobulin chl genes and their hypermutation.
A:Reference number: S40312; MID:94080891
A:Accession: S40328
A>Status: preliminary; translation not shown
A:Molecule type: mRNA
A:Residues: 1-131 <KLE>
C:Cross-references: EMBL:X72438; NID:g441344; PIDN:CAA5106.1; PID:g441345
C:Superfamily: Immunoglobulin V region; Immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:35-109/Domain: immunoglobulin homology <IM>

Query Match          91.4%; Score 562; DB 2; Length 131;
Best Local Similarity 89.7%; Pred. No. 5.9e-40;
Matches 105; Conservative 5; Mismatches 7; Indels 0; Gaps 0;

OY    1 LMLPDTGTGIWVTOSPATLTVSPGERATLTSCRASQSVSSNLAWYOOKPGQAPRLLITYGAS 60
DB    12 LMLPTGTGEVMTOSPATLTVSPGERATLTSCRASQSVHINLAWYOOKPGQAPRLLITYGAY 71

OY    61 TRATGTPARFSGSGSGETFTLTITSSLOSDEFAVYYCOQYNMPPYFGGTLEIKR 117
DB    72 TRATGTPARFSGSGSGETFTLTITSSLOSDELTATYYCOQYNDMPWTFCGGTVEIKR 128

F:RT      4
SA40378
IG kappa chain - human
C:Species: Homo sapiens (man)
C>Date: 06-Mar-1994 #sequence_revision 26-May-1995 #text_change 21-Jan-2000
Accession: S40378
R:Klein, R.; Jaenichen, R.; Zachau, H.G.
Eur. J. Immunol. 23, 3248-3271, 1993
A>Title: Expressed human immunoglobulin chl genes and their hypermutation.
A:Reference number: S40312; MID:94080891
A:Accession: S40378
A>Status: preliminary; translation not shown
A:Molecule type: mRNA
A:Residues: 1-123 <KLE>
C:Cross-references: EMBL:X72488; NID:g441444; PIDN:CAA5115.1; PID:g441445
C:Superfamily: Immunoglobulin V region; Immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:29-103/Domain: immunoglobulin homology <IM>

Query Match          87.7%; Score 539.5; DB 2; Length 123;
Best Local Similarity 87.3%; Pred. No. 4e-36;
Matches 103; Conservative 6; Mismatches 8; Indels 1; Gaps 1;

OY    1 LMLPTGTGIWVTOSPATLTVSPGERATLTSCRASQSVSSNLAWYOOKPGQAPRLLITYGAS 60

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```

Db      6 IWLPGTGTGIVMTQSPATLTVSPGDATILSCASAGVSSNLAWYHRGQAAPRLIYTGS 65
Oy      61 TTAATIPARFSGSGSGTEFTLTITSSLOSEDFRAYVYCQOYNMWP- YTGOGKLEIKR 117
       ||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      66 TTAATIPARFSGSGSGTEFTLTITSSLOSADPAIYYCQOYIDMPWYTRFGQGRILDIKR 123
       ||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

RESULT      5
A56701
Ig kappa chain V region precursor (Hva) - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 19-Oct-1995 #sequence_revision 19-Oct-1995 #text_change 21-Jan-2000
C:Accession: A56701
R:Nickerson, K.G.; Tao, M.H.; Chen, H.T.; Larrick, J.; Kabat, E.A.
J. Biol. Chem. 270, 12457-12465, 1995
A:title: Human and mouse monoclonal antilpodies to blood group A substance, which are
A:Reference number: A56701; MUID:95279371
A:Accession: A56701
A:Status: Preliminary
A:Molecule type: mRNA
A:Residues: 1-128 <NIC>
A:Cross-references: GB:I411174; NID:g762823; PID:A564877.1; PID:g762824
C:Superfamily: Immunoglobulin V region; Immunoglobulin homology
C:Keywords: heterotetramer; Immunoglobulin
F:36-110/Domain: Immunoglobulin homology <IMM>

Query Match      86.3%; Score 530.5; DB 2; Length 128;
Best Local Similarity 88.0%; Pred. No. 2,3e-37;
Matches 103; Conservative 7; Mismatches 6; Indels 1; Gaps 1;

Oy      1 IWLPTGEIYVTQSPATLVSPGERATLSGRASVSNSLAWTOQRGAAPRLIYTGS 60
       ||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      13 IWLPTGEIYLTOSPATLISPGERATLSGRASVSNSYLAWYOQRGAAPRLIYTDS 72
       ||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

Oy      61 TRATGIPARFSGSGSGTEFTLTITSSLOSEDFRAYVYCQOYNMWPPTFGOKLEIKR 117
       ||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      73 NRATGIPARFSGSGSGTDFTLTITSLPEDEFAVYICQQRSMW-PKSFQGKVEIKR 128
       ||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

RESULT      6
K3HDC1
Ig kappa chain precursor V-III region (CLL) - human
N:Alternate names: rheumatoid factor
C:Species: Homo sapiens (man)
C:Date: 04-Dec-1986 #sequence_revision 04-Dec-1986 #text_change 21-Jan-2000
C:Accession: A01898
R:Jirik, F.R.; Soergel, J.; Fong, S.; Helzlsouer, J.G.; Curd, J.G.; Chen, P.P.; Goldfien
Proc. Natl. Acad. Sci. U.S.A. 83, 2195-2199, 1986
A:title: Cloning and sequence determination of a human rheumatoid factor light-chain
A:Reference number: A01898; MUID:66177570
A:Accession: A01898
A:Molecule type: DNA
A:Residues: 1-115 <JIR>
C:Note: The sequence was determined from the germline gene
C:Genetics:
A:Gene: GDB:IGKV3
A:Cross-references: GDB:136266
A:Map position: 2P12-2p11
A:Inserts: 17/1
C:Complex: An immunoglobulin heterotetramer subunit consists of two identical light (L)
chain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into
C:Superfamily: Immunoglobulin V region; Immunoglobulin homology
C:Keywords: autoantibody; chronic lymphocytic leukemia; heterotetramer; immunoglobulin<IG>
F:21-115/Product: rheumatoid factor, Ig kappa chain V-III region (CLL) #status predic
F:21-43/Region: framework 1
F:36-110/Domain: Immunoglobulin homology <IMM>
F:44-54/Region: complementarity-determining 1
F:55-69/Region: framework 2
F:70-76/Region: complementarity-determining 2
F:77-108/Region: framework 3
F:109-115/Region: complementarity-determining 3

```


F:43-108/Disulfide Bonds: #status predicted

Query Match 85.78; Score 527; DB 1; Length 115;

Best Local Similarity 97.18; Pred. No. 4,1e-37; Mismatches 2; Indels 0; Gaps 0;

Matches 100; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Db 13 LMLPDTGELVMTQSPATLSVSPGERATLSCRASQSVSNLAWYQKPGQAPRLIYGAS 60
13 LMLPDTGELVMTQSPATLSVSPGERATLSCRASQSVSNLAWYQKPGQAPRLIYGAS 72

RESULT 7

Ig kappa chain V region - human

C:Species: Homo sapiens (man)
C:Date: 02-Dec-1993 #sequence_revision 10-Nov-1995 #text_change 21-Jan-2000

C:Accession: S34005; S30524

R:Marlette, X.; Tsapis, A.; Broquet, J.C.

E: Eur. J. Immunol. 23, 846-851, 1993

A:Title: Nucleotide sequence analysis of the variable domains of four human monoclonal

A:Reference number: S34001; MUID:93209281

A:Accession: S34005

A:Status: Preliminary

A:Molecule type: mRNA

A:Residues: 1-107 <NAR>

A:Cross-references: EMBL:218330

C:Superfamily: Immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

F:16-90/Domain: immunoglobulin homology <IMM>

Query Match 85.68; Score 526.5; DB 2; Length 107;
Best Local Similarity 96.38; Pred. No. 4,2e-37;
Matches 104; Conservative 1; Mismatches 2; Indels 1; Gaps 1;Db 9 EIVMTQSPATLSVSPGERATLSCRASQSVSNLAWYQKPGQAPRLIYGAS 68
1 EIVMTQSPATLSVSPGERATLSCRASQSVSNLAWYQKPGQAPRLIYGAS 60Cy 69 RFSSGSGTEFTLTISLSQSDPAFYVYCOQYNNMPYFGGKLEIK 116
61 RFSSGSGTEFTLTISLSQSDPAFYVYCOQYNNMPYFGGKLEIK 107

RESULT 8

Ig kappa chain precursor V-III region (Hah) - human (fragment)

C:Species: Homo sapiens (man)
C:Date: 03-Mar-1989 #sequence_revision 03-Mar-1989 #text_change 21-Jan-2000

C:Accession: A30553

R: Liu, M.F.; Robbins, D.L.; Crowley, J.J.; Sinha, S.; Kozin, F.; Kipps, T.J.; Carson, D.

J. Immunol. 142, 688-694, 1989
A:Title: Characterization of four homologous L chain variable region genes that are reA:Reference number: A30553; MUID:89093959
A:Accession: A30553
A:Status: Preliminary
A:Molecule type: DNA
A:Residues: 1-115 <LUD>
A:Note: The sequence was determined from the differentiated gene
C:Superfamily: Immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:36-110/Domain: immunoglobulin homology <IMM>

Query Match 85.78; Score 527; DB 1; Length 115;

Best Local Similarity 97.18; Pred. No. 4,1e-37; Mismatches 2; Indels 0; Gaps 0;

Matches 100; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Db 13 LMLPDTGELVMTQSPATLSVSPGERATLSCRASQSVSNLAWYQKPGQAPRLIYGAS 60
13 LMLPDTGELVMTQSPATLSVSPGERATLSCRASQSVSNLAWYQKPGQAPRLIYGAS 72Cy 61 TRATGIPARFSGSGGTEFTLTISLSQSDPAFYVYCOQYNNMP 103
73 TRATGIPARFSGSGGTEFTLTISLSQSDPAFYVYCOQYNNMP 115

RESULT 9

Ig kappa chain precursor V-J-C region (LS1) - human (fragment)

C:Species: Homo sapiens (man)
C:Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 21-Jan-2000

C:Accession: PLO106

R: Silberstein, L.E.; Litwin, S.; Carmack, C.E.

J. Exp. Med. 169, 1631-1643, 1989

A:Title: Relationship of variable region genes expressed by a human B cell lymphoma s

A:Reference number: PLO106; MUID:89235583

A:Accession: PLO106

A:Molecule type: mRNA

A:Residues: 1-144 <STL>

C:Superfamily: Immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

F:1-20/Domain: signal sequence #status predicted <Sig>

F:21-115/Domain: V region <VRE>

F:36-110/Domain: immunoglobulin homology <IMM>

F:44-54/Region: complementarity-determining 1

F:70-76/Region: complementarity-determining 2

F:109-115/Region: complementarity-determining 3

F:116-127/Domain: J region <JRG>

F:128-144/Domain: C region (fragment) <CRE>

Query Match 85.48; Score 525.5; DB 2; Length 144;
Best Local Similarity 87.28; Pred. No. 6,7e-37;
Matches 102; Conservative 7; Mismatches 7; Indels 1; Gaps 1;Db 13 LMLPDTGELVMTQSPATLSVSPGERATLSCRASQSVSNLAWYQKPGQAPRLIYGAS 60
13 LMLPDTGELVMTQSPATLSVSPGERATLSCRASQSVSNLAWYQKPGQAPRLIYGAS 72Cy 61 TRATGIPARFSGSGGTEFTLTISLSQSDPAFYVYCOQYNNMPYFGGKLEIK 117
73 TRATGIPARFSGSGGTEFTLTISLSQSDPAFYVYCOQYNNMPYFGGKLEIK 128

RESULT 10

Ig kappa chain V-III region (Ger) - human

C:Species: Homo sapiens (man)
C:Date: 05-Jun-1988 #sequence_revision 05-Jun-1988 #text_change 21-Jan-2000

C:Accession: B26555

R: Madaugh, C.R.; Litman, G.W.

J. Biol. Chem. 262, 3671-3673, 1987

A:Title: Atypical glycosylation of an IgG monoclonal cryoimmunoglobulin.

A:Reference number: A92630; MUID:87137666

A:Accession: B26555

A:Status: Preliminary

A:Molecule type: protein

A:Residues: 1-116 <MID>

C:Superfamily: Immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

F:16-90/Domain: immunoglobulin homology <IMM>

OY 69 RFGSGSGTEFTLTSSLOSEDFAYVYCOQYNNMPYFGGKLEIKR 117
 |||||||
 DB 61 RFGSGSGTEFTLTSSLOSEDFAYVYCOQYNNMPYFGGKLEIKR 109

RESULT 11

Ig kappa chain V-J region - human
 S40326
 C:Species: Homo sapiens (man)
 C>Date: 19-May-1994 #sequence_revision 26-May-1995 #text_change 21-Jan-2000
 C:Accession: S40326
 R:Klein, R.; Jaenichen, R.; Zachau, H.G.
 Eur. J. Immunol. 23, 3248-3271, 1993
 A:Title: Expressed human immunoglobulin chl genes and their hypermutation.
 A:Reference number: S40312; MUID:94080891
 A:Accession: S40326
 A:Status: preliminary; translation not shown
 A:Molecule type: mRNA
 A:Residues: 1-110 <KLB>
 A:Cross-references: EMBL:X72436
 C:Superfamily: immunoglobulin V region; immunoglobulin homology
 C:Keywords: heterotetramer; immunoglobulin
 F:32-106/Domain: immunoglobulin homology <IMM>

Query Match 84.9%; Score 522; DB 2; Length 110;
 Best Local Similarity 100.0%; Pred. No. 1e-36;
 Matches 101; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 LMLPDTGELVMTQSPATLSVSPGERATLSCRASQSVSNLAWYQOKPGQAPRLITYGAS 60
 |||||||
 DB 9 LMLPDTGELVMTQSPATLSVSPGERATLSCRASQSVSNLAWYQOKPGQAPRLITYGAS 68
 |||||||
 OY 61 TRATGIPARFSSGSGTEFTLTSSLOSEDFAYVYCOQYNN 101
 |||||||
 DB 69 TRATGIPARFSSGSGTEFTLTSSLOSEDFAYVYCOQYNN 109

RESULT 12

S40379
 Ig kappa chain V-J region - human
 C:Species: Homo sapiens (man)
 C>Date: 19-May-1994 #sequence_revision 26-May-1995 #text_change 21-Jan-2000
 C:Accession: S40379
 R:Klein, R.; Jaenichen, R.; Zachau, H.G.
 Eur. J. Immunol. 23, 3248-3271, 1993
 A:Title: Expressed human immunoglobulin chl genes and their hypermutation.
 A:Reference number: S40312; MUID:94080891
 A:Accession: S40379
 A:Status: preliminary; translation not shown
 A:Molecule type: mRNA
 A:Residues: 1-128 <KLB>
 A:Cross-references: EMBL:X72489; NID:g441446; PIDN:CA51157.1; PID:g441447
 C:Superfamily: immunoglobulin V region; immunoglobulin homology
 C:Keywords: heterotetramer; immunoglobulin
 F:36-110/Domain: immunoglobulin homology <IMM>

Query Match 84.3%; Score 518.5; DB 2; Length 128;
 Best Local Similarity 85.5%; Pred. No. 2.3e-36;
 Matches 100; Conservative 8; Mismatches 8; Indels 1; Gaps 1;

OY 1 LMLPDTGELVMTQSPATLSVSPGERATLSCRASQSVSNLAWYQOKPGQAPRLITYGAS 60
 |||||||
 DB 13 LMLPDTGELVMTQSPATLSVSPGERATLSCRASQSVSNLAWYQOKPGQAPRLITYGAS 72
 |||||||
 OY 61 TRATGIPARFSSGSGTEFTLTSSLOSEDFAYVYCOQYNNMPYFGGKLEIKR 117
 |||||||
 DB 73 NRATGIPARFSSGSGTEFTLTSSLOSEDFAYVYCOQYNNMPYFGGKLEIKR 128

RESULT 13

JE0244

Ig kappa chain NIG2 precursor - human
 C:Species: Homo sapiens (man)
 C>Date: 05-Dec-1998 #sequence_revision 05-Dec-1998 #text_change 21-Jan-2000
 C:Accession: JE0244
 R:Alim, M.A.; Hara, Y.; Hossein, M.S.; Takeda, K.; Yamagata, F.; Yamaki, S.; Kazi, H.
 submitted to JIPID, November 1998
 A:Description: A new subgroup of k type light chains (KV) identified in cases of AL
 A:Reference number: JE0243
 A:Accession: JE0244
 A:Molecule type: protein
 A:Residues: 1-215 <AL>
 C:Superfamily: immunoglobulin V region; immunoglobulin homology
 F:16-90/Domain: immunoglobulin homology <IMM>

Query Match 83.6%; Score 514; DB 2; Length 215;
 Best Local Similarity 89.9%; Pred. No. 8.8e-36;
 Matches 98; Conservative 5; Mismatches 6; Indels 0; Gaps 0;

OY 9 EIVMTQSPATLSVSPGERATLSCRASQSVSNLAWYQOKPGQAPRLITYGASTRATGIPA 68
 |||||||
 DB 1 EVLVQSPATLSVSPGERATLSCRASQSVSNLAWYQOKPGQAPRLITYRASTRATGIPA 60
 |||||||
 OY 69 RFGSGSGTEFTLTSSLOSEDFAYVYCOQYNNMPYFGGKLEIKR 117
 |||||||
 DB 61 RFGSGSGTEFTLTSSLOSEDFAYVYCOQYNNMPYFGGKLEIKR 109

RESULT 14

S29627
 Ig kappa chain V region (60.3 hybridoma) - human
 C:Species: Homo sapiens (man)
 C>Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 21-Jan-2000
 C:Accession: S34110; S29627
 R:Walls, M.A.; Hsiao, K.; Harris, L.J.
 Nucleic Acids Res. 21, 2921-2929, 1993
 A:Title: Vectors for the expression of PCR-amplified immunoglobulin variable domains
 A:Reference number: S34110; MUID:93324379
 A:Accession: S34110
 A:Status: nucleic acid sequence not shown; translation not shown
 A:Molecule type: mRNA
 A:Residues: 1-129 <MA>
 A:Cross-references: EMBL:L17330; NID:g38511; PIDN:CA79978.1; PID:g38512
 A>Note: human sequences cloned and sequenced prior to expression in mouse myeloma cell
 C:Genetics: 17/1
 C:Superfamily: immunoglobulin V region; immunoglobulin homology
 C:Keywords: heterotetramer; immunoglobulin
 F:36-110/Domain: immunoglobulin homology <IMM>

Query Match 83.5%; Score 513.5; DB 2; Length 129;
 Best Local Similarity 85.5%; Pred. No. 5.9e-36;
 Matches 100; Conservative 6; Mismatches 10; Indels 1; Gaps 1;

OY 1 LMLPDTGELVMTQSPATLSVSPGERATLSCRASQSVSNLAWYQOKPGQAPRLITYGAS 60
 |||||||
 DB 13 LMLPDTGELVMTQSPATLSVSPGERATLSCRASQSVSNLAWYQOKPGQAPRLITYGAS 72
 |||||||
 OY 61 TRATGIPARFSSGSGTEFTLTSSLOSEDFAYVYCOQYNNMPYFGGKLEIKR 116
 |||||||
 DB 73 NRATGIPARFSSGSGTEFTLTSSLOSEDFAYVYCOQYNNMPYFGGKLEIKR 129

RESULT 15

S46375
 Ig kappa chain V-J region (733-5) - human (fragment)
 C:Species: Homo sapiens (man)
 C>Date: 27-Jan-1995 #sequence_revision 01-Sep-1995 #text_change 21-Jan-2000
 C:Accession: S46375; S38648
 R:Bensimon, C.; Chastagner, P.; Zouali, M.
 EMBO J. 13, 2951-2962, 1994

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GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: July 26, 2000, 14:25:25 ; Search time 12.18 Seconds
(without alignments)
237.679 Million cell updates/sec

Title: US-09-203-768a-4
Perfect score: 1 LMDPTGELVMTGSPATLS.....QYNNPPYFGGCTKLEIKR 117
Sequence: 615

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Search: 85661 seqs, 30989116 residues
Total number of hits satisfying chosen parameters: 85661

Minimum DB seq length: 0
Maximum DB seq length: 1000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SWISSProt_38.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description |
|------------|-------|-------------|--------|----|--------------------|
| 1 | 591 | 96.1 | 129 | 1 | P04207 homo sapien |
| 2 | 510 | 82.9 | 129 | 1 | P18135 homo sapien |
| 3 | 509 | 82.8 | 129 | 1 | P18136 homo sapien |
| 4 | 504 | 82.0 | 109 | 1 | P01624 homo sapien |
| 5 | 493.5 | 80.2 | 128 | 1 | P06311 homo sapien |
| 6 | 489 | 79.5 | 115 | 1 | P04433 homo sapien |
| 7 | 458.5 | 74.6 | 116 | 1 | P04434 homo sapien |
| 8 | 454 | 73.8 | 109 | 1 | P01620 homo sapien |
| 9 | 449 | 73.0 | 109 | 1 | P01622 homo sapien |
| 10 | 448 | 72.8 | 109 | 1 | P01623 homo sapien |
| 11 | 440 | 71.5 | 108 | 1 | P01618 homo sapien |
| 12 | 435.5 | 70.8 | 108 | 1 | P01605 homo sapien |
| 13 | 429.5 | 69.8 | 134 | 1 | P06314 homo sapien |
| 14 | 428 | 69.6 | 109 | 1 | P04206 homo sapien |
| 15 | 421 | 68.5 | 133 | 1 | P06313 homo sapien |
| 16 | 415.5 | 67.6 | 114 | 1 | P01625 homo sapien |
| 17 | 414.5 | 67.4 | 100 | 1 | P01621 homo sapien |
| 18 | 404.5 | 65.8 | 108 | 1 | P01604 homo sapien |
| 19 | 396.5 | 64.5 | 108 | 1 | P01610 homo sapien |
| 20 | 395.5 | 64.3 | 108 | 1 | P04430 homo sapien |
| 21 | 395.5 | 64.3 | 131 | 1 | P01661 mus musculu |
| 22 | 394.5 | 64.1 | 108 | 1 | P01600 homo sapien |
| 23 | 394 | 64.1 | 117 | 1 | P01602 homo sapien |
| 24 | 389.5 | 63.3 | 149 | 1 | P01633 mus musculu |
| 25 | 389 | 63.3 | 107 | 1 | P01598 homo sapien |
| 26 | 386.5 | 62.8 | 108 | 1 | P01598 homo sapien |
| 27 | 384.5 | 62.5 | 132 | 1 | P01658 mus musculu |
| 28 | 382.5 | 62.2 | 108 | 1 | P01609 homo sapien |
| 29 | 381.5 | 62.0 | 108 | 1 | P01599 homo sapien |
| 30 | 380.5 | 61.9 | 108 | 1 | P01603 homo sapien |
| 31 | 380 | 61.8 | 121 | 1 | P06312 homo sapien |
| 32 | 379.5 | 61.7 | 129 | 1 | P04431 homo sapien |
| 33 | 378.5 | 61.5 | 108 | 1 | P01594 homo sapien |

| | | | | | | |
|----|-------|------|-----|---|------------|--------------------|
| 34 | 378.5 | 61.5 | 108 | 1 | KV1Y_HUMAN | P03622 homo sapien |
| 35 | 377.5 | 61.4 | 108 | 1 | KV1C_HUMAN | P01595 homo sapien |
| 36 | 371 | 60.3 | 112 | 1 | KV3B_MOUSE | P01655 mus musculu |
| 37 | 370.5 | 60.2 | 108 | 1 | KV1O_HUMAN | P01607 homo sapien |
| 38 | 370.5 | 60.2 | 111 | 1 | KV3M_MOUSE | P01665 mus musculu |
| 39 | 370.5 | 60.2 | 136 | 1 | KV3L_MOUSE | P01654 mus musculu |
| 40 | 369.5 | 60.1 | 111 | 1 | KV3L_MOUSE | P01664 mus musculu |
| 41 | 368.5 | 59.9 | 111 | 1 | KV3H_MOUSE | P01660 mus musculu |
| 42 | 368 | 59.8 | 133 | 1 | KV2E_HUMAN | P06310 homo sapien |
| 43 | 367.5 | 59.8 | 108 | 1 | KV1S_HUMAN | P01611 homo sapien |
| 44 | 367.5 | 59.8 | 111 | 1 | KV3O_MOUSE | P01667 mus musculu |
| 45 | 366.5 | 59.6 | 111 | 1 | KV3J_MOUSE | P01662 mus musculu |

ALIGNMENTS

| RESULT | ID | QUERY | STANDARD | PRT | AA |
|-------------------------------|--|---|----------|-----|----|
| 1 | KV3H_HUMAN | | | | |
| AC | P04207 | 20-MAR-1987 (Rel. 04, Created) | | | |
| DT | 01-NOV-1990 (Rel. 16, Last sequence update) | | | | |
| DE | IG KAPPA CHAIN V-III REGION CXL PRECURSOR (RHEDMATAID FACTOR). | | | | |
| OS | Homo sapiens (Human) | | | | |
| OC | Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; | | | | |
| CC | Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo. | | | | |
| CC | [1] | | | | |
| RP | SEQUENCE FROM N.A. | | | | |
| RX | MEDLINE: 86177570. | | | | |
| RA | Jirik F.R., Sore J., Fong S., Heltmann J.G., Cud J.G., Chen P.P., | | | | |
| RT | Goldfien R., Carson D.A., "Cloning and sequence determination of a human rheumatoid factor | | | | |
| RL | light-chain gene." | | | | |
| Proc. Natl. Acad. Sci. U.S.A. | 83:2195-2199(1986). | | | | |
| CC | ----- | | | | |
| CC | This SWISS-PROT entry is copyright. It is produced through a collaboration | | | | |
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| CC | or send an email to license@isb-sib.ch). | | | | |
| CC | ----- | | | | |
| DR | EMBL: M12740; AA58992.1; - | | | | |
| DR | PIR: A01898; K3HUC1. | | | | |
| DR | HSSP: P01789; 2MCP. | | | | |
| DR | PFAM: PF00047; 1g; 1. | | | | |
| KW | Immunoglobulin V region; Signal. | | | | |
| FT | SIGNAL | 1 | 20 | | |
| FT | CHAIN | 21 | 129 | | |
| FT | DOMAIN | 21 | 43 | | |
| FT | DOMAIN | 44 | 54 | | |
| FT | DOMAIN | 55 | 69 | | |
| FT | DOMAIN | 70 | 76 | | |
| FT | DOMAIN | 77 | 108 | | |
| FT | DOMAIN | 109 | 118 | | |
| FT | DOMAIN | 119 | 129 | | |
| FT | DISULFID | 43 | 108 | | |
| FT | NOV TER | 129 | 129 | | |
| SO | SEQUENCE | 129 AA; 14275 MW; 5C13B411BE60CC14 CRC64; | | | |
| Query Match | 96.1%; Score 591; DB 1; Length 129; | | | | |
| Best Local Similarity | 94.9%; Pred. No. 6,3e-51; | | | | |
| Matches | 111; Conservative 4; Mismatches 2; Indels 0; Gaps 0; | | | | |
| OY | 1 LMDPTGELVMTGSPATLSVSPERATLSCRASQSVSNLAWYQQRPGAPRLILYGAS 60 | | | | |
| DB | 13 LMDPTGELVMTGSPATLSVSPERATLSCRASQSVSNLAWYQQRPGAPRLILYGAS 72 | | | | |
| OY | 61 TRAGIPARFSGSGSGTEFTLTISLSQSEDPAYVYCCQYNNPPYTTGGGCTKLEIKR 117 | | | | |

Db 73 TRATGIPARFSSGSGTEFTLITSLRLOSEDFAYVYCCQYNNWPMPTGCGTRVEIKR 129

RESULT 2

ID KV3L HUMAN STANDARD; PRT; 129 AA.

AC P18135;

DT 01-NOV-1990 (Rel. 16, Created)

DT 01-NOV-1990 (Rel. 16, Last sequence update)

DE 15-JUL-1999 (Rel. 38, Last annotation update)

DE IG KAPPA CHAIN V-II REGION HAH PRECURSOR.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

RN Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

RP SEQUENCE FROM N.A.

RX MEDLINE; 88171307.

RK Kipps T.J., Tomhave E., Chen P.P., Carson D.A.;

"Autoclonal antibody-associated kappa light chain variable region gene

expressed in chronic lymphocytic leukemia with little or no somatic

mutation. Implications for etiology and immunotherapy.";

J. Exp. Med. 167:840-852(1988).

-1- DISEASE: THE PROTEIN IS ONE OF THE SURFACE IMMUNOGLOBULIN M

AUTOANTIBODIES EXPRESSED IN PATIENTS WITH CHRONIC LYMPHOCYTIC

LEUKEMIA.

PIR; P10022; K3HUA.

DR HSSP; P01789; 2MCP.

DR PFAM; PF00047; 19; 1.

KW Immunoglobulin V region; Signal.

FT SIGNAL 1 20

FT CHAIN 21 129

FT DOMAIN 21 43

FT DOMAIN 44 55

FT DOMAIN 56 70

FT DOMAIN 71 77

FT DOMAIN 78 109

FT DOMAIN 110 118

FT DOMAIN 119 129

FT DISULFID 43 109

FT NON TER 129 129

SO SEQUENCE 129 AA; 14073 MW; D3C53292772774D0 CRC64;

Query Match 82.9%; Score 510; DB 1; Length 129;

Best Local Similarity 85.6%; Pred. No. 4.7e-43;

Matches 101; Conservative 7; Mismatches 8; Indels 2; Gaps 2;

Db 13 LWPDTGELVMTQSPATLSVSPGERATLSCRASQSVSSN-LAWYQKPGQAPRLIYGA 72

QY 60 STRATGIPARFSSGSGTEFTLITSLRLOSEDFAYVYCCQYNNWPMPTGCGTRVEIKR 117

DB 73 SSRATGIPRFSGSGTDTLTITSLRLEPDFAVYCCQYGT-SPTFGGTRVEIKR 129

RESULT 3

ID KV3N HUMAN STANDARD; PRT; 129 AA.

AC P18136;

DT 01-NOV-1990 (Rel. 16, Created)

DT 01-NOV-1990 (Rel. 16, Last sequence update)

DE 15-JUL-1999 (Rel. 38, Last annotation update)

DE IG KAPPA CHAIN V-II REGION HIC PRECURSOR.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

RN Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

RP SEQUENCE FROM N.A.

RX MEDLINE; 88171307.

RA Kipps T.J., Tomhave E., Chen P.P., Carson D.A.;

"Autoclonal antibody-associated kappa light chain variable region gene

RT expressed in chronic lymphocytic leukemia with little or no somatic

mutation. Implications for etiology and immunotherapy.";

J. Exp. Med. 167:840-852(1988).

-1- DISEASE: THE PROTEIN IS ONE OF THE SURFACE IMMUNOGLOBULIN M

AUTOANTIBODIES EXPRESSED IN PATIENTS WITH CHRONIC LYMPHOCYTIC

LEUKEMIA.

PIR; P10021; K3HUI.

DR HSSP; P01789; 2MCP.

DR PFAM; PF00047; 19; 1.

KW Immunoglobulin V region; Signal.

FT SIGNAL 1 20

FT CHAIN 21 129

FT DOMAIN 21 43

FT DOMAIN 44 55

FT DOMAIN 56 70

FT DOMAIN 71 77

FT DOMAIN 78 109

FT DOMAIN 110 118

FT DOMAIN 119 129

FT DISULFID 43 109

FT NON TER 129 129

SO SEQUENCE 129 AA; 14070 MW; 7395528EA2B74D6 CRC64;

Query Match 82.8%; Score 509; DB 1; Length 129;

Best Local Similarity 84.7%; Pred. No. 5.9e-43;

Matches 100; Conservative 9; Mismatches 7; Indels 2; Gaps 2;

Db 13 LWPDTGELVMTQSPATLSVSPGERATLSCRASQSVSSN-LAWYQKPGQAPRLIYGA 72

QY 60 STRATGIPARFSSGSGTEFTLITSLRLOSEDFAYVYCCQYNNWPMPTGCGTRVEIKR 117

DB 73 SSRATGIPRFSGSGTDTLTITSLRLEPDFAVYCCQYGT-SPTFGGTRVEIKR 129

RESULT 4

ID KV3F HUMAN STANDARD; PRT; 109 AA.

AC P01624;

DT 21-JUL-1986 (Rel. 01, Created)

DT 21-JUL-1986 (Rel. 01, Last sequence update)

DE 15-JUL-1999 (Rel. 38, Last annotation update)

DE IG KAPPA CHAIN V-II REGION POW.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

RN Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

RP SEQUENCE.

RX MEDLINE; 76276460.

RA Klapper D.G., Capra J.D.;

"The amino acid sequence of the variable regions of the light chains

from two idiotypically cross reactive Igm anti-gamma globulins.";

Ann. Inst. Pasteur Immunol. 127C:261-271(1976).

-1- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM AN IGM WITH ANTI-GAMMA

GLOBULIN ACTIVITY.

PIR; A01897; K3HUP.

DR HSSP; P01789; 2MCP.

DR PFAM; PF00047; 19; 1.

KW Immunoglobulin V region.

FT DISULFID 23 89

FT NON TER 109 109

SO SEQUENCE 109 AA; 11922 MW; 62821DDC6A8A86 CRC64;

Query Match 82.0%; Score 504; DB 1; Length 109;

Best Local Similarity 90.9%; Pred. No. 1.5e-42;

Matches 100; Conservative 4; Mismatches 4; Indels 2; Gaps 2;

QY 9 EIVMTQSPATLSVSPGERATLSCRASQSVS-SNLAWYQKPGQAPRLIYGA STRATGIP 67

DB 1 EIVMTQSPATLSVSPGERATLSCRASQSVSISNSYLAWYQKPGSGPRLIYGA STRATGIP 60

OY 68 ARFGSSGTEFTLTISSLOSEDFAVYCCOQYNNMPPYFGGTLEIKR 117
 DB 61 ARFGSSGTEFTLTISSLOSEDFAVYCCOQYNNMPPYFGGTLEIKR 109

RESULT 5

KV3J_HUMAN STANDARD; PRT; 128 AA.

AC P06311;

DT 01-JAN-1988 (Rel. 06, Created)

DT 01-JAN-1988 (Rel. 06, Last sequence update)

DT 15-JUL-1999 (Rel. 38, Last annotation update)

DE IG KAPPA CHAIN V-II REGION IARC/BL41 PRECURSOR.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.

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CC or send an email to license@isb-sib.ch).

CC EMBL; Z00021; CAAT7316.1; -

DR PIR; A01899; K3H041.

DR PIR; PF00047; 19; 1.

DR Immunoglobulin V region; Signal.

FT CHAIN 1 20

FT SIGNAL 21 128

FT DOMAIN 21 43

FT DOMAIN 44 54

FT DOMAIN 55 69

FT DOMAIN 70 76

FT DOMAIN 77 108

FT DOMAIN 109 117

FT DOMAIN 118 128

FT DISULFID 43 108

FT NON_TER 128 128

SEQUENCE 128 AA; 14070 MW; CC8957F0FE3B9012 CRC64;

Query Match 80.2%; Score 493.5; DB 1; Length 128;

Best Local Similarity 82.9%; Pred. No. 1.9e-41;

Matches 97; Conservative 7; Mismatches 12; Indels 1; Gaps 1;

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.

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CC or send an email to license@isb-sib.ch).

CC EMBL; X01668; -; NOT_ANNOTATED_CDS.

DR PIR; A01900; K3H041.

DR PIR; PF00047; 19; 1.

DR Immunoglobulin V region; Signal.

FT CHAIN 1 20

FT SIGNAL 21 115

FT DOMAIN 21 43

FT DOMAIN 44 54

FT DOMAIN 55 69

FT DOMAIN 70 76

FT DOMAIN 77 108

FT DOMAIN 109 115

FT DISULFID 43 108

FT NON_TER 115 115

SEQUENCE 115 AA; 12575 MW; 2DE47CDA3A17D555 CRC64;

Query Match 79.5%; Score 489; DB 1; Length 115;

Best Local Similarity 90.3%; Pred. No. 4.5e-41;

Matches 93; Conservative 5; Mismatches 5; Indels 0; Gaps 0;

OY 1 LMLPDTGEIYVTOGSPATLSVSPERATLSCRASOSVSSNLAWYQKRGAPRLIYGAS 60

DB 13 LMLPDTGEIYVTOGSPATLSVSPERATLSCRASOSVSSNLAWYQKRGAPRLIYGAS 72

OY 61 TRAGCIPARFSGSGTEFTLTISSLOSEDFAVYCCOQYNNMPPYFGGTLEIKR 103

DB 73 TRAGCIPARFSGSGTEFTLTISSLOSEDFAVYCCOQYNNMPPYFGGTLEIKR 115

RESULT 7

KV3J_HUMAN STANDARD; PRT; 116 AA.

AC P04434;

DT 13-AUG-1987 (Rel. 05, Created)

DT 13-AUG-1987 (Rel. 05, Last sequence update)

DT 15-JUL-1999 (Rel. 38, Last annotation update)

DE IG KAPPA CHAIN V-II REGION VH PRECURSOR (FRAGMENT).

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.

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or send an email to license@slb.ch).

CC EMBL: X02725; -; NOT_ANNOTATED_CDS.

DR PIR: A01901; K3HUVH.

DR HSSP: P01789; 2MCP.

DR PFAM: PF00047; 19; 1.

DR Immunoglobulin V region; Signal.

FT CHAIN 1 20 IG KAPPA CHAIN V-III REGION VH.

FT SIGNAL 21 >116 FRAMEWORK 1. DETERMINING 1.

FT DOMAIN 21 43 COMPLEMENTARITY-DETERMINING 1.

FT DOMAIN 44 55 FRAMEWORK 2.

FT DOMAIN 56 70 COMPLEMENTARITY-DETERMINING 2.

FT DOMAIN 71 77 FRAMEWORK 3.

FT DOMAIN 78 109 COMPLEMENTARITY-DETERMINING 3.

FT DISULFID 110 116 BY SIMILARITY.

FT NON_TER 43 109 BY SIMILARITY.

FT SEQUENCE 116 AA; 12757 MW; 51CD5BA53B21929 CRC64;

Query Match 74.6%; Score 458.5; DB 1; Length 116;

Best Local Similarity 87.5%; Pred. No. 4.2e-38;

Matches 91; Conservative 4; Mismatches 8; Indels 1; Gaps 1;

QY 1 LMLPDTGEIVMTQSPATLSVSPGERATLSCRASQSVSSN-LAMYQKPGQAPRLIYGA 59

DB 13 LMLPDTREIVMTQSPATLSVSPGERATLSCRASQSVSSN-LAMYQKPGQAPRLIYGA 72

QY 60 STRATGIPARFSGSGSTFTLTISLQSEDFAVYCCQYNNMP 103

DB 73 STRATGIPARFSGSGSTFTLTISLQSEDFAVYCCQYNNMP 116

RESULT 8

KV3B_HUMAN STANDARD; PRT; 109 AA.

AC P01620;

DT 21-JUL-1986 (Rel. 01, Created)

DT 21-JUL-1986 (Rel. 01, Last sequence update)

DT 15-JUL-1999 (Rel. 38, Last annotation update)

DE IG KAPPA CHAIN V-III REGION SITE.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.

RP SEQUENCE.

RA MEDLINE: 82046598.

RA Andrews D.W., Capra J.D.;

RT "Amino acid sequence of the variable regions of light chains from two

RT idiotypically cross-reactive human IgM anti-gamma-globulins of the Wa

RT group."

RL Biochemistry 20:5816-5822(1981).

CC -1- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM AN IGM WITH ANTI-GAMMA

CC GLOBULIN ACTIVITY.

CC PIR: A01892; K3HUSI.

DR HSSP: P01789; 2MCP.

DR PFAM: PF00047; 19; 1.

DR Immunoglobulin V region.

FT DISULFID 23 89 BY SIMILARITY.

FT NON_TER 109 109 BY SIMILARITY.

FT SEQUENCE 109 AA; 11775 MW; 7689C3BCD646FFB4 CRC64;

Query Match 73.8%; Score 454; DB 1; Length 109;

Best Local Similarity 82.7%; Pred. No. 1.1e-37;

Matches 91; Conservative 9; Mismatches 8; Indels 2; Gaps 2;

QY 9 EIVMTQSPATLSVSPGERATLSCRASQSVSSN-LAMYQKPGQAPRLIYGASTRATGIP 67

DB 1 EIVMTQSPATLSVSPGERATLSCRASQSVSSN-LAMYQKPGQAPRLIYGASTRATGIP 60

QY 68 ARFSGSGSTFTLTISLQSEDFAVYCCQYNNMPYFGGCTKLEIKR 117

DB 68 ARFSGSGSTFTLTISLQSEDFAVYCCQYNNMPYFGGCTKLEIKR 117

FT SEQUENCE 109 AA; 11775 MW; 7689C3BCD646FFB4 CRC64;

Query Match 73.8%; Score 454; DB 1; Length 109;

Best Local Similarity 82.7%; Pred. No. 1.1e-37;

Matches 91; Conservative 9; Mismatches 8; Indels 2; Gaps 2;

QY 9 EIVMTQSPATLSVSPGERATLSCRASQSVSSN-LAMYQKPGQAPRLIYGASTRATGIP 67

DB 1 EIVMTQSPATLSVSPGERATLSCRASQSVSSN-LAMYQKPGQAPRLIYGASTRATGIP 60

DB 61 DRFSGSGSTFTLTISLQSEDFAVYCCQYNNMPYFGGCTKLEIKR 109

RESULT 9

KV3D_HUMAN STANDARD; PRT; 109 AA.

AC P01622;

DT 21-JUL-1986 (Rel. 01, Created)

DT 21-JUL-1986 (Rel. 01, Last sequence update)

DT 15-JUL-1999 (Rel. 38, Last annotation update)

DE IG KAPPA CHAIN V-III REGION TI.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.

RP SEQUENCE.

RA MEDLINE: 72188439.

RA Suter L., Barnikol H.U., Watanabe S., Hilschmann N.;

RT "Rule of antibody structure. The primary structure of a monoclonal

RT immunoglobulin L-chain of kappa-type, subgroup 3 (Bence-Jones protein

RT ti). IV. The complete amino acid sequence and its significance for

RT the mechanism of antibody production."

RL Hope-Seyler's Z. Physiol. Chem. 353:189-208(1972).

CC -1- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (3) MARKER.

CC -1- MISCELLANEOUS: THIS IS A BENCE-JONES PROTEIN.

DR PIR: A01895; K3HUTI.

DR HSSP: P01789; 2MCP.

DR PFAM: PF00047; 19; 1.

DR Immunoglobulin V region; Bence-Jones protein.

FT DISULFID 23 89 BY SIMILARITY.

FT NON_TER 109 109 BY SIMILARITY.

FT SEQUENCE 109 AA; 11788 MW; 8C35058C0C7749BC CRC64;

Query Match 73.0%; Score 449; DB 1; Length 109;

Best Local Similarity 81.8%; Pred. No. 3.3e-37;

Matches 90; Conservative 10; Mismatches 8; Indels 2; Gaps 2;

QY 9 EIVMTQSPATLSVSPGERATLSCRASQSVSSN-LAMYQKPGQAPRLIYGASTRATGIP 67

DB 1 EIVMTQSPATLSVSPGERATLSCRASQSVSSN-LAMYQKPGQAPRLIYGASTRATGIP 60

QY 68 ARFSGSGSTFTLTISLQSEDFAVYCCQYNNMPYFGGCTKLEIKR 117

DB 61 DRFSGSGSTFTLTISLQSEDFAVYCCQYNNMPYFGGCTKLEIKR 109

RESULT 10

KV3E_HUMAN STANDARD; PRT; 109 AA.

AC P01623;

DT 21-JUL-1986 (Rel. 01, Created)

DT 21-JUL-1986 (Rel. 01, Last sequence update)

DT 15-JUL-1999 (Rel. 38, Last annotation update)

DE IG KAPPA CHAIN V-III REGION MOL.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.

RP SEQUENCE.

RA MEDLINE: 82046598.

RA Andrews D.W., Capra J.D.;

RT "Amino acid sequence of the variable regions of light chains from two

RT idiotypically cross-reactive human IgM anti-gamma-globulins of the Wa

RT group."

RL Biochemistry 20:5816-5822(1981).

CC -1- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM AN IGM WITH ANTI-GAMMA

CC GLOBULIN ACTIVITY.

CC PIR: A01896; K3HUTL.

DR HSSP: P01789; 2MCP.

DR PFAM: PF00047; 19; 1.

DR Immunoglobulin V region.

FT DISULFID 23 89 BY SIMILARITY.

FT NON_TER 109 109
SQ SEQUENCE 109 AA: 11746 MW: 566C115E6B9CBECE CRC64;

Query Match 72.8%; Score 448; DB 1; Length 109;
Best Local Similarity 82.7%; Pred. No. 4, 1e-37;
Matches 91; Conservative 7; Mismatches 10; Indels 2; Gaps 2;

OY 9 EIVMTQSPATLSVSPGERATLSCRASQSVSSN-LAWYQOKPGQAPRLIYGASTRATGIP 67
DB 1 EIVLQSPGTLISPEERATLSCRASQSVSSGTLGWYQOKPGQAPRLIYGASTRATGIP 60

OY 68 ARFSGSGSTFTLTSSLOSEDFAVYVCOQYNNMPYFGQGTKEIKR 117
DB 61 DRFSGSGSTFTLTSSLOSEDFAVYVCOQYNNMPYFGQGTKEIKR 109

RESULT 11
KV3A_HUMAN STANDARD; PRT; 108 AA.
P01619;

DI 21-JUL-1986 (rel. 01, Created)
DT 21-JUL-1986 (rel. 01, Last sequence update)
DT 15-JUL-1999 (rel. 38, Last annotation update)
DE IG KAPPA CHAIN V-III REGION B6.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
RN Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
[1]

RP SEQUENCE.
RA Milstein C.;
RT "The basic sequences of immunoglobulin kappa chains: sequence studies
of Bence Jones proteins Rad. F4 and B6.";
RL FEBS Lett. 2:301-304(1969).
CC -1- MISCELLANEOUS: THIS IS A BENCE-JONES PROTEIN.
DR HSSP; P01789; 2MCP.
DR PFAM; PF00047; 19; 1.
KW Immunoglobulin V region; Bence-Jones protein.
FT DISULFID 23 89 BY SIMILARITY.
FT NON_TER 108 108
SQ SEQUENCE 108 AA: 11635 MW: 8BC14FE07A419E3D CRC64;

Query Match 71.5%; Score 440; DB 1; Length 108;
Best Local Similarity 77.1%; Pred. No. 2, 4e-36;
Matches 84; Conservative 13; Mismatches 10; Indels 2; Gaps 2;

OY 9 EIVMTQSPATLSVSPGERATLSCRASQSVSSN-LAWYQOKPGQAPRLIYGASTRATGIP 67
DB 1 ZIVLTSPGTLISPEERATLSCRASQSVSSGTLGWYQOKPGQAPRLIYGASTRATGIP 60

OY 68 ARFSGSGSTFTLTSSLOSEDFAVYVCOQYNNMPYFGQGTKEIKR 116
DB 61 DRFSGSGSTFTLTSSLOSEDFAVYVCOQYNNMPYFGQGTKEIKR 108

RESULT 12
KV1M_HUMAN STANDARD; PRT; 108 AA.
P01605;

DI 21-JUL-1986 (rel. 01, Created)
DT 21-JUL-1986 (rel. 01, Last sequence update)
DT 15-JUL-1999 (rel. 38, Last annotation update)
DE IG KAPPA CHAIN V-I REGION IAY.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
RN Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
[1]

RP SEQUENCE.
RA MEDLINE; 77038198.
RA Capra J.D., Klapper D.G.;
KW "Complete amino acid sequence of the variable domains of two human

RT Igm anti-gamma globulins (Iay/Pom) with shared idiotypic
RT specificities.";
RL Scand. J. Immunol. 5:677-684(1976).

CC -1- MISCELLANEOUS: THE SECOND AND THIRD HYPERVARIABLE REGIONS OF THIS
CHAIN ARE IDENTICAL WITH THOSE OF THE HUMAN POM V-III KAPPA CHAIN,
WITH WHICH IT SHARES CERTAIN IDIOTYPIC DETERMINANTS.
CC -1- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM AN IGM WITH ANTI-GAMMA
GLOBULIN ACTIVITY.
DR PIR; A01871; KIHITL.

DR HSSP; P01607; 1RET.
DR PFAM; PF00047; 19; 1.
KW Immunoglobulin V region.

FT DOMAIN 1 23 FRAMEWORK 1.
FT DOMAIN 24 34 COMPLEMENTARITY-DETERMINING 1.
FT DOMAIN 35 49 FRAMEWORK 2.
FT DOMAIN 50 56 COMPLEMENTARITY-DETERMINING 2.
FT DOMAIN 57 88 FRAMEWORK 3.
FT DOMAIN 89 97 COMPLEMENTARITY-DETERMINING 3.
FT DOMAIN 98 107 FRAMEWORK 4.
FT DISULFID 23 88 BY SIMILARITY.
FT NON_TER 108 108
SQ SEQUENCE 108 AA: 11834 MW: 73993A95431434A CRC64;

Query Match 70.8%; Score 435.5; DB 1; Length 108;
Best Local Similarity 73.4%; Pred. No. 6, 7e-36;
Matches 80; Conservative 16; Mismatches 12; Indels 1; Gaps 1;

OY 9 EIVMTQSPATLSVSPGERATLSCRASQSVSSN-LAWYQOKPGQAPRLIYGASTRATGIP 68
DB 1 DIQMTQSPATLSVSPGERATLSCRASQSVSSGTLGWYQOKPGQAPRLIYGASTRATGIP 60

OY 69 ARFSGSGSTFTLTSSLOSEDFAVYVCOQYNNMPYFGQGTKEIKR 117
DB 61 DRFSGSGSTFTLTSSLOSEDFAVYVCOQYNNMPYFGQGTKEIKR 108

RESULT 13
KV4C_HUMAN STANDARD; PRT; 134 AA.
P06314;

DI 01-JAN-1988 (rel. 06, Created)
DT 01-APR-1988 (rel. 07, Last sequence update)
DT 15-JUL-1999 (rel. 38, Last annotation update)
DE IG KAPPA CHAIN V-IV REGION B17 PRECURSOR.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
RN Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
[1]

RP SEQUENCE FROM N.A.
RA Marsh P., Mills F., Gould H.;
RT "Detection of a unique human V kappa IV germline gene by a cloned
cDNA probe.";
RL Nucleic Acids Res. 13:6531-6544(1985).
RN [2]

RP REVISION TO 76.
RA Marsh P.;
RL Submitted (OCT-1986) to the EMBL/GenBank/DBJ databases.

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DR EMBL; X02990; GA26733.1; -
DR PIR; A01905; K4HUI7.
DR HSSP; P01789; 2MCP.
DR PFAM; PF00047; 19; 1.
KW Immunoglobulin V region; Signal.

FT SIGNAL 1 20
 FT CHAIN 21 134 IG KAPPA CHAIN V-IV REGION B17.
 FT DOMAIN 21 43 FRAMEWORK 1.
 FT DOMAIN 44 60 COMPLEMENTARITY-DETERMINING 1.
 FT DOMAIN 61 75 FRAMEWORK 2.
 FT DOMAIN 76 82 COMPLEMENTARITY-DETERMINING 2.
 FT DOMAIN 83 114 FRAMEWORK 3.
 FT DOMAIN 115 121 COMPLEMENTARITY-DETERMINING 3.
 FT DOMAIN 122 133 FRAMEWORK 4.
 FT DISULFID 43 114 BY SIMILARITY.
 FT NON_TER 134 134
 SQ SEQUENCE 134 AA; 14966 MW; 6413A22ED0738832 CRC64;

Query Match 69.88; Score 429.5; DB 1; Length 134;
 Best Local Similarity 69.98; Pred. No. 3.3e-35;
 Matches 86; Conservative 16; Mismatches 14; Indels 7; Gaps 3;

1 LMPDPTGEIYMTQSPATLSVSGERATLSCRASQSV--SSN---LAWYQKPGQAPRL 54
 13 LMIAGAGDIYMTQSPDLSVSGERATLSCRASQSV--SSN---LAWYQKPGQAPRL 72
 55 LIYAGSTRATGIPARFSGSGSGTEFTLTISLSQSEDFAVYVCOQYNNMPYTFGQGTLE 114
 73 LIYASTRESGVDPDRFSGSGSGTEFTLTISLSQSEDFAVYVCOQYNNMPYTFGQGTLE 131
 115 IKR 117
 132 IKR 134

RESULT 14
 KV3G_HUMAN
 ID KV3G_HUMAN STANDARD; PRT; 109 AA.
 AC P04206; 20-MAR-1987 (Rel. 04, Created)
 DT 20-MAR-1987 (Rel. 04, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE IG KAPPA CHAIN V-III REGION GOL (RHEUMATOID FACTOR).
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 RN [1]
 RP MEDLINE; 86230578.
 RA Newkirk M., Chen P.P., Carson D.A., Posnett D., Capra J.D.;
 "Amino acid sequence of a light chain variable region of a human
 rheumatoid factor of the Wa idiotype group, in part predicted by its
 reactivity with anti-peptide antibodies.";
 RL Mol. Immunol. 23:239-244(1986).
 DR PIR: A01893; K3HUGO.
 DR HSSP: P01789; 2MCP.
 DR PRAM: PF00047; 19; 1.
 KW Immunoglobulin V region.
 FT DISULFID 23 89
 FT NON_TER 109 109 BY SIMILARITY.
 SQ SEQUENCE 109 AA; 11830 MW; 9349A5BD9358B6 CRC64;

Query Match 69.68; Score 428; DB 1; Length 109;
 Best Local Similarity 78.28; Pred. No. 3.6e-35;
 Matches 86; Conservative 10; Mismatches 12; Indels 2; Gaps 2;

9 EIVMTQSPATLSVSGERATLSCRAS--OSVSNLAWYQKPGQAPRLIYAGSTRATGIP 67
 1 EIVMTQSPATLSVSGERATLSCRAS--OSVSNLAWYQKPGQAPRLIYAGSTRATGIP 60
 68 ARFSGSGSGTEFTLTISLSQSEDFAVYVCOQYNNMPYTFGQGTLEIKR 117
 61 DRFSGSGSGTEFTLTISLSQSEDFAVYVCOQYNNMPYTFGQGTLEIKR 109

RESULT 15

KV4B_HUMAN
 ID KV4B_HUMAN STANDARD; PRT; 133 AA.
 AC P06313; 01-JAN-1988 (Rel. 06, Created)
 DT 01-JAN-1988 (Rel. 06, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE IG KAPPA CHAIN V-IV REGION JI PRECURSOR.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 RN [1]
 RP SEQUENCE FROM N.A.
 RA MEDLINE; 86041853.
 RA Klobbeck H.G., Bornkamm G.W., Combriato G., Mochkat R., Pohlenz H.D.,
 RT "Subgroup IV of human immunoglobulin K light chains is encoded by a
 single germ-line gene";
 RL Nucleic Acids Res. 13:6515-6529(1985).
 CC -----
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 CC -----
 DR EMBL; Z00022; CAA77317.1; .
 DR PIR: A01904; K4HUII.
 DR HSSP: P01789; 2MCP.
 DR PRAM: PF00047; 19; 1.
 KW Immunoglobulin V region; Signal.
 FT SIGNAL 1 20
 FT CHAIN 21 133 IG KAPPA CHAIN V-IV REGION JI.
 FT DOMAIN 21 43 FRAMEWORK 1.
 FT DOMAIN 44 60 COMPLEMENTARITY-DETERMINING 1.
 FT DOMAIN 61 75 FRAMEWORK 2.
 FT DOMAIN 76 82 COMPLEMENTARITY-DETERMINING 2.
 FT DOMAIN 83 114 FRAMEWORK 3.
 FT DOMAIN 115 122 COMPLEMENTARITY-DETERMINING 3.
 FT DOMAIN 123 132 FRAMEWORK 4.
 FT DISULFID 43 114 BY SIMILARITY.
 FT NON_TER 133 133
 SQ SEQUENCE 133 AA; 14632 MW; 5FB395306744AF4 CRC64;

Query Match 68.58; Score 421; DB 1; Length 133;
 Best Local Similarity 69.98; Pred. No. 2.2e-34;
 Matches 86; Conservative 15; Mismatches 14; Indels 8; Gaps 3;

1 LMPDPTGEIYMTQSPATLSVSGERATLSCRASQSV--SSN---LAWYQKPGQAPRL 54
 13 LMIAGAGDIYMTQSPDLSVSGERATLSCRASQSV--SSN---LAWYQKPGQAPRL 72
 55 LIYAGSTRATGIPARFSGSGSGTEFTLTISLSQSEDFAVYVCOQYNNMPYTFGQGTLE 114
 73 LIYASTRESGVDPDRFSGSGSGTEFTLTISLSQSEDFAVYVCOQYNNMPYTFGQGTLE 130
 115 IKR 117
 131 IKR 133

Search completed: July 26, 2000, 14:25:25
 Job time: 1331 sec

Wed Jul 26 15:40:47 2000

us-09-203-768a-4.rsp

Page 7

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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: July 26, 2000, 14:25:01 ; Search time 48.79 Seconds
(without alignments)
166.265 Million cell updates/sec

Title: US-09-203-768a-4
Perfect score: 615
Sequence: 1 LMLPDTGTGEIVMTQSPATLS.....QYNNMPYTEGQTKLEIKR 117

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 225878 segs, 69334122 residues

Number of hits satisfying chosen parameters: 225878

Minimum DB seg length: 0
Maximum DB seg length: 1000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :
1: SP-archaea:*
2: SP-bacteria:*
3: SP-fungi:*
4: SP-human:*
5: SP-invertebrate:*
6: SP-mammal:*
7: SP-mhc:*
8: SP-organelle:*
9: SP-phage:*
10: SP-plant:*
11: SP-rodent:*
12: SP-virus:*
13: SP-vertebrate:*
14: SP-unclassified:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|-------|-------------|--------|-------|-------------|
| 1 | 145 | 23.6 | 123 | 11 | 061243 |
| 2 | 123 | 20.0 | 235 | 6 | 09XSM6 |
| 3 | 120.5 | 19.6 | 210 | 6 | P79336 |
| 4 | 120 | 19.5 | 147 | 4 | 09Y509 |
| 5 | 117.5 | 19.1 | 397 | 4 | 09Y4V0 |
| 6 | 117 | 19.0 | 503 | 4 | P78324 |
| 7 | 115.5 | 18.8 | 398 | 4 | 000241 |
| 8 | 114 | 18.5 | 209 | 6 | 09XSM7 |
| 9 | 109.5 | 17.8 | 118 | 11 | 09Z1C4 |
| 10 | 108.5 | 17.6 | 136 | 13 | 09YHR9 |
| 11 | 108 | 17.6 | 100 | 6 | 077624 |
| 12 | 107 | 17.4 | 150 | 4 | 09Y298 |
| 13 | 105.5 | 17.2 | 506 | 6 | 046631 |
| 14 | 105 | 17.1 | 228 | 11 | 070153 |
| 15 | 104 | 16.9 | 198 | 4 | 013970 |
| 16 | 103 | 16.7 | 700 | 4 | 075054 |
| 17 | 102.5 | 16.7 | 142 | 11 | 09YH02 |
| 18 | 102 | 16.6 | 513 | 13 | P97797 |
| 19 | 101.5 | 16.5 | 136 | 13 | 09YH02 |

| | | | | | | |
|----|-------|------|------|----|--------|--------------------|
| 20 | 100.5 | 16.3 | 140 | 13 | 09YH09 | 09YH09 ginglymosto |
| 21 | 99 | 16.1 | 2222 | 5 | 097394 | 097394 drosophila |
| 22 | 98.5 | 16.0 | 122 | 4 | 099604 | 099604 homo sapien |
| 23 | 98.5 | 16.0 | 133 | 13 | 09YH04 | 09YH04 ginglymosto |
| 24 | 98.5 | 16.0 | 506 | 6 | 046632 | 046632 bos taurus |
| 25 | 97.5 | 15.9 | 122 | 4 | 099603 | 099603 homo sapien |
| 26 | 97.5 | 15.9 | 143 | 13 | 09YH07 | 09YH07 ginglymosto |
| 27 | 97 | 15.8 | 100 | 13 | 09YH10 | 09YH10 ginglymosto |
| 28 | 96.5 | 15.7 | 136 | 13 | 09YH04 | 09YH04 ginglymosto |
| 29 | 96.5 | 15.7 | 318 | 13 | 09YH01 | 09YH01 xenopus lae |
| 30 | 96.5 | 15.7 | 100 | 13 | 09YH01 | 09YH01 ginglymosto |
| 31 | 96 | 15.6 | 138 | 13 | 09YH07 | 09YH07 ginglymosto |
| 32 | 96 | 15.6 | 142 | 13 | 09YH03 | 09YH03 ginglymosto |
| 33 | 96 | 15.6 | 157 | 4 | 095978 | 095978 homo sapien |
| 34 | 95.5 | 15.5 | 144 | 13 | 09YH09 | 09YH09 ginglymosto |
| 35 | 95.5 | 15.5 | 134 | 13 | 09YH08 | 09YH08 ginglymosto |
| 36 | 94.5 | 15.4 | 136 | 13 | 09YH03 | 09YH03 ginglymosto |
| 37 | 94.5 | 15.4 | 137 | 13 | 09YH00 | 09YH00 ginglymosto |
| 38 | 94.5 | 15.4 | 152 | 13 | 09YH00 | 09YH00 ginglymosto |
| 39 | 94 | 15.3 | 138 | 13 | 09YH00 | 09YH00 ginglymosto |
| 40 | 93.5 | 15.2 | 235 | 13 | 090770 | 090770 gallus gall |
| 41 | 93.5 | 15.2 | 97 | 4 | 043234 | 043234 homo sapien |
| 42 | 93 | 15.1 | 97 | 4 | 09YH05 | 09YH05 ginglymosto |
| 43 | 93 | 15.1 | 101 | 13 | 09YH06 | 09YH06 ginglymosto |
| 44 | 93 | 15.1 | 131 | 13 | 09YH17 | 09YH17 ginglymosto |
| 45 | 93 | 15.1 | 131 | 13 | 09YH17 | 09YH17 ginglymosto |

ALIGNMENTS

RESULT 1
ID 061243 PRELIMINARY; PRT; 123 AA.
AC 061243;
DT 01-NOV-1996 (TRENDELREL. 01, Created)
DT 01-NOV-1996 (TRENDELREL. 01, Last sequence update)
DT 01-NOV-1999 (TRENDELREL. 12, Last annotation update)
DE 8HS20 PROTEIN PRECURSOR.
GN VPRED3.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia;
OC Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-BALB/C;
RX MEDLINE; 93259124.
RA SHIRASAWA T., OHNISHI K., HAGIWARA S., SHIGEMOTO K., TAKEBE Y.,
RA RAJESKRY K., TAKEMORI T.;
RT "A novel gene product associated with mu chains in immature B cells."
RL EMBL J.12:1827-1834(1993).
DR EMBL; D13208; BAA02495.1; -;
DR MGD; MGI:98938; Vpred3.
DR PFM; PFM00047; 19; 1.
FT CHAIN
SQ SEQUENCE 123 AA; 13400 MW; DA2A70D3 CRC32;
8HS20 PROTEIN.
Query Match 23.6%; Score 145; DB 11; Length 123;
Best Local Similarity 40.2%; Pred. No. 6,46-08;
Matches 41; Conservative 13; Mismatches 38; Indels 10; Gaps 5;
QY 12 MTQSPATLSVSPGERATISCRASQSVSS---NLAWYQKRGQARRLITYGAST---RAT 64
DB 23 LITQ-PDASVFPQGDPAHSLCTINSQAHATAGDIGVSWYQOPGSAPHLITYAAEEHYPRA 81
QY 65 GIPARFSGS--GSGTEFTLTSSLOSEDFAYVYCCQYNNMPP 104
DB 82 DIPDRFSATVDAAHNACTILITSPVLPEDDADYFCISATIFEP 123
RESULT 2
Q9XSM6

| ID | 09XSM6: | PRELIMINARY: | PRT: | 235 AA. |
|----|---|---|-----------|-----------------|
| AC | 01-NOV-1999 | (TREMblrel. 12, Created) | | |
| DT | 01-NOV-1999 | (TREMblrel. 12, Last sequence update) | | |
| DT | 01-NOV-1999 | (TREMblrel. 12, Last annotation update) | | |
| DE | CD8 ALPHA CHAIN PRECURSOR. | | | |
| OS | Salimiri sciureus (Common squirrel monkey). | | | |
| OC | Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; | | | |
| OC | Eutheria; Primates; Platyrrhini; Cebidae; Cebinae; Salimiri. | | | |
| RM | [1] | | | |
| RP | SEQUENCE FROM N.A. | | | |
| RC | STRAIN-92039; | | | |
| RX | MEDLINE: 99299362. | | | |
| RA | UREA-TYDAD A., GARCIA Z., LEMONNIER F.A., KAZANJI M.; | | | |
| RT | "Molecular characterization of cDNAs encoding squirrel monkey (Salimiri | | | |
| RL | sciureus) CD8 alpha and beta chains."; | | | |
| DB | Immunogenetics 49:718-721(1999). | | | |
| DB | EMBL: AJ130818; CABA1462.1; - | | | |
| DB | Signal. | | | |
| ET | SIGNAL. | | | |
| ET | CHAIN | 1 | 21 | POTENTIAL. |
| ET | CHAIN | 22 | 235 | CD8 ALPHA CHAIN |
| SO | SEQUENCE | 235 AA: | 25728 MW; | F22E0A05 CRC32; |

| | | | | |
|-----------------------|--------|--------------------|----------------|-------------|
| Query Match | 20.0%; | Score 123; | DB 6; | Length 235; |
| Best Local Similarity | 35.0%; | Pred. No. 2.5e-05; | | |
| Matches | 35; | Conservative 12; | Mismatches 39; | Indels 14; |
| | | | | Gaps 5 |

[illegible]

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RESULT 3
P79336
ID P79336 PRELIMINARY; PRT; 210 AA.
AC P79336;
DT 01-MAY-1997 (TREMBLrel. 03, Created)
DT 01-MAY-1997 (TREMBLrel. 03, Last sequence update)
DT 01-JAN-1999 (TREMBLrel. 09, Last annotation update)
DE CDB BETA ANTIGEN PRECURSOR.
FE Felis silvestris catus (Cat).
OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
   Carnivora; Felidae; Felis.
   [1]
RN 1]
RP SEQUENCE FROM N.A.
RC TISSUE=THYMOS;
RA MYAZAWA T.;
RL Submitted (JAN-1997) to the EMBL/genbank/DBJ databases.
   [2]
RP SEQUENCE FROM N.A.
RC TISSUE=THYMOS;
RX MEDLINE; 97067796.
RA PECORARO M.R., SHIMOJIMA M., MAEDA K., INOSHIMA Y., KAWAGUCHI Y.
   KAI C., MIKAMI T.;
   "Molecular cloning of the feline CD8 beta-chain.";
   Immunology 89:84-88(1996).
   EMBL; AB000484; BAA19125.1; -.
DR PFM; PFM0047; Ig; 1.
KW Signal.
FT SIGNAL
FT CHAIN 1 21 POTENTIAL.
FT SEQUENCE 210 AA; 23105 MW; 915E2BD1 CRC32;

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| | | | | |
|-----------------------|--------|------------------|--------|----------------|
| Query Match | 19.6%; | Score 120.5; | DB 6; | Length 210; |
| Best Local Similarity | 23.7%; | Pred. No. 4e-05; | | |
| Matches | 32; | Conservative | 25; | Mismatches 53; |
| | | | Indels | 25; |
| | | | Gaps | 5 |

```

0Y 1 LMPDPT-----GEIYATGSPATLVSPPGRATLSGRASG-VSSNLATYQXKPGGAP- 52
Db 5 LMLLATATLAALRSSSVYQXQPGSWMYQTNGVMIMSEAKTSPTSTRIRYMLRHRQAPSPD 64
0Y 53 -----RLTIYGASPRATGTPARFGSGSGTEFTLTISLSQSDPAVYYCCQYN 100
Db 65 SHYECLAWMDPIKIGYVGOEVE----PEKLTVPDADRSLIINTSVKPADSGIYFCMTVG 120
0Y 101 NMPPTFGGQTKLEI 115
Db 121 S-PELTFRGKTRLSY 134

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| RESULT | 4 | |
|--------|---|---|
| 09Y509 | | |
| ID | 09Y509 | PRELIMINARY; PRT; 147 AA. |
| AC | 09Y509; | |
| DT | 01-NOV-1999 | (TREMBLrel. 12, Created) |
| DT | 01-NOV-1999 | (TREMBLrel. 12, last sequence update) |
| DT | 01-NOV-1999 | (TREMBLrel. 12, last annotation update) |
| DE | VH3 PROTEIN (FRAGMENT). | |
| GN | VH3. | |
| OS | Homio sapiens (Human). | |
| OC | Eumetazoa; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; | |
| OC | Euthelia; Primates; Catarrhini; Homnidae; Homo. | |
| RN | [1] | |
| RP | SEQUENCE FROM N.A. | |
| RX | MEDLINE; 96071149. | |
| RA | CAO J., VESCOIO R.A., RETTING M.B., HONG C.H., KIM A., LEE J.C., | |
| RA | LICHTENSTEIN A.K., BERENSON J.R.; | |
| RT | "A CD10-positive subset of malignant cells is identified in multiple | |
| RT | myeloma using PCR with patient-specific immunoglobulin gene primers." | |
| RL | Leukemia 9:1948-1993(1995). | |
| DR | EMBL; S80860; AAD14339.1; -. | |
| FT | NON_TER | |
| Q0 | SEQUENCE | 147 AA; 15768 MW; BDD08F70 CRC32; |

| | | | | |
|-----------------------|-------|------------------|--------|----------------|
| Query Match | 19.5% | Score 120; | DB 4; | length 147; |
| Best Local Similarity | 32.7% | Pred. No. 3e-05; | | |
| Matches | 37; | Conservative | 19; | Mismatches 39; |
| | | | Indels | 18; |
| | | | Gaps | 5. |

| RESULT | 5 | |
|--------|--|--|
| 09X4V0 | | |
| ID | 09X4V0 | PRELIMINARY; |
| AC | 09X4V0 | PRT; 397 AA. |
| DT | 01-NOV-1999 | (TEMBIREI. 12, Created) |
| DT | 01-NOV-1999 | (TEMBIREI. 12, last sequence update) |
| DT | 01-NOV-1999 | (TEMBIREI. 12, last annotation update) |
| DE | DJ576H24.2 | (SIRP-BETAL (SIGNAL REGULATORY PROTEIN BETA 1)). |
| GN | DJ576H24.2 | |
| OS | Homo sapiens (Human) | |
| OC | Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia | |
| OC | Eutheria; Primates; Catarrhini; Hominoidea; Homo. | |
| RN | [1] | |
| RP | SEQUENCE FROM N.A. | |
| RA | MATTHEWS L. | |
| RL | Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases. | |
| DR | EMBL; AL049634; C646661.1; - | |
| DQ | SEQUENCE 397 AA; 43037 MW; C9D81FC5 CRC32; | |

| | | | | |
|-----------------------|--------|--------------------|-------|-------------|
| Query Match | 19.18; | Score 117.5; | DB 4; | Length 397; |
| Best Local Similarity | 24.28; | Pred. No. 0.00017; | | |

Matches 30; Conservative 23; Mismatches 44; Indels 27; Gaps 4;

OY 9 EIVMTOSPATLSVSPGERLTSCRASQSVS-SNLAW-----YQKPGCAPRLI 56
 DB 31 ELQVTPDKSVVAAGESLILHCVTSLIPGPIWFRGAGARELLINQKGEHPRYTT 90
 OY 57 YGASTRANGIPARFGSGSGTEFTLISLSQSEDAVYVCOQYNNWMP---YTFGQGT 112
 DB 91 VELTKRNNL-----DFSISISNITPADAGTYCVAFRFGSPDVEFKSGAGTE 139
 OY 113 LEIK 116
 DB 140 LSVR 143

RESULT 6
 P78324 PRELIMINARY; PRT; 503 AA.

ID P78324
 AC 000683;
 01-NOV-1998 (TREMBLrel. 08, last sequence update)
 01-NOV-1998 (TREMBLrel. 08, last sequence update)
 01-NOV-1998 (TREMBLrel. 12, last sequence update)
 DE PROTEIN TITROSINE PHOSPHATASE, NON-RECEPTOR TYPE SUBSTRATE 1 PRECURSOR
 DE (SHP SUBSTRATE-1) (INHIBITORY RECEPTOR SHPS-1) (SIGNAL-
 DE REGULATORY PROTEIN ALPHA-1) (SIRP-ALPHA1) (MYD-1 ANTIGEN).
 GN PTENS1 OR SHPS-1 OR DJ684024.1.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
 OC Eutheria; Primates; Catarrhini; Homidae; Homo.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE-BRAIN;
 RX MEDLINE: 97223399.
 RA YAMAO T., MATOZAKI T., AMANO K., MATSUDA Y., TAKAHASHI N., OCHI F.,
 RA FUJIOKA Y., KASUGA M.;
 RT "Mouse and human SHPS-1: molecular cloning of cDNAs and chromosomal
 RT localization of genes."
 RL Biochem. Biophys. Res. Commun. 231:61-67(1997).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE-PLACENTA;
 RX MEDLINE: 97215901.
 RA KHARITONENKOV A., CHEN Z., SURES I., WANG H., SCHILLING J.,
 RA ULRICH A.;
 RT "A family of proteins that inhibit signalling through tyrosine kinase
 RT receptors."
 RL Nature 386:181-186(1997).
 RN [3]
 RP SEQUENCE OF 146-503 FROM N.A.
 RC BATES K.;
 RL Submitted (MAR-1999) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: BINDS TO THE SH2 DOMAINS OF PROTEIN-TYROSINE PHOSPHATASE
 CC 2C (SHP-2) AFTER TYROSINE PHOSPHORYLATION INDUCED BY VARIOUS
 CC MITOGENS AND CELL ADHESION. MAY ACT AS A DOCKING PROTEIN AND
 CC INDUCE TRANSLLOCATION OF SHP-2 FROM THE CYTOSOL TO THE PLASMA
 CC MEMBRANE.
 CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
 CC -1- TISSUE SPECIFICITY: WIDELY EXPRESSED WITH HIGHEST LEVELS IN BRAIN.
 CC HIGH LEVELS ALSO PRESENT IN HEART, SPLEEN, TESTIS, OVARY AND
 CC PERIPHERAL BLOOD LEUKOCYTES.
 CC -1- SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY. CONTAINS
 CC TWO C1-LIKE AND ONE V-LIKE DOMAINS.
 DR EMBL: D86043; BAA12974.1;
 DR EMBL: Y10375; CAA71403.1;
 DR EMBL: AL034362; CAB3874.1;
 DR MIM: 602461;
 DR PFMW: PF00047.1; 3.
 KW Signal; Transmembrane; Alternative splicing; Immunoglobulin domain;
 KW Glycoprotein; SH3-binding; Phosphorylation.
 FT SIGNAL 1 26
 FT CHAIN 27 503
 FT DOMAIN 27 372
 FT EXTRACELLULAR (POTENTIAL).

FT TRANSMEM 373 393 POTENTIAL.
 FT DOMAIN 394 503 CYTOPLASMIC (POTENTIAL).
 FT DOMAIN 43 129 IG-LIKE V-TYPE DOMAIN.
 FT DOMAIN 164 233 IG-LIKE C1-TYPE DOMAIN.
 FT DOMAIN 266 339 IG-LIKE C1-TYPE DOMAIN.
 FT DOMAIN 428 431 SH2-BINDING (POTENTIAL).
 FT DOMAIN 438 443 SH3-BINDING (POTENTIAL).
 FT DOMAIN 452 455 SH2-BINDING (POTENTIAL).
 FT DOMAIN 469 472 SH2-BINDING (POTENTIAL).
 FT DOMAIN 495 498 SH2-BINDING (POTENTIAL).
 FT MOD_RES 428 428 PHOSPHORYLATION (POTENTIAL).
 FT MOD_RES 452 452 PHOSPHORYLATION (POTENTIAL).
 FT MOD_RES 469 469 PHOSPHORYLATION (POTENTIAL).
 FT MOD_RES 495 495 PHOSPHORYLATION (POTENTIAL).
 FT CARBOHYD 244 244 POTENTIAL.
 FT CARBOHYD 269 269 POTENTIAL.
 FT CARBOHYD 291 291 POTENTIAL.
 FT CARBOHYD 318 318 POTENTIAL.
 SQ SEQUENCE 503 AA; 54812 MW; 0CA5272E CRC32;

Query Match 19.0%; Score 117; DB 4; Length 503;
 Best Local Similarity 24.4%; Pred. No. 0.00025;
 Matches 30; Conservative 23; Mismatches 44; Indels 26; Gaps 4;

OY 9 EIVMTOSPATLSVSPGERLTSCRASQSVS-SNLAW-----YQKPGCAPRLI 56
 DB 33 ELQVTPDKSVVAAGESLILHCVTSLIPGPIWFRGAGARELLINQKGEHPRYTT 92
 OY 57 YGASTRANGIPARFGSGSGTEFTLISLSQSEDAVYVCOQYNNWMP---YTFGQGT 113
 DB 93 VESTKRENN-----DFSISISNITPADAGTYCVAFRFGSPDTEKSGAGTEL 141
 OY 114 LEIK 116
 DB 142 SVR 144

RESULT 7
 000241 PRELIMINARY; PRT; 398 AA.

ID 000241
 AC 000241;
 01-NOV-1998 (TREMBLrel. 08, last sequence update)
 01-NOV-1998 (TREMBLrel. 08, last sequence update)
 01-NOV-1998 (TREMBLrel. 11, last sequence update)
 DE SIGNAL-REGULATORY PROTEIN BETA-1 PRECURSOR (SIRP-BETA1).
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
 OC Eutheria; Primates; Catarrhini; Homidae; Homo.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE-PLACENTA;
 RA KHARITONENKOV A., CHEN Z., SURES I., WANG H., SCHILLING J.,
 RA ULRICH A.;
 RL Nature 386:181-186(1997).
 CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
 CC -1- SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY. CONTAINS
 CC TWO C1-LIKE AND ONE V-LIKE DOMAINS.
 DR EMBL: Y10376; CAA71404.1;
 DR PFMW: PF00047.1; 3.
 KW Signal; Immunoglobulin domain; Glycoprotein; Transmembrane.
 FT SIGNAL 1 26
 FT CHAIN 27 398
 FT DOMAIN 27 371
 FT DOMAIN 372 392
 FT TRANSMEM 372 392
 FT DOMAIN 393 398
 FT DOMAIN 42 128
 FT DOMAIN 163 233
 FT DOMAIN 267 338
 FT CARBOHYD 102 102
 FT CARBOHYD 244 244
 FT CARBOHYD 269 269
 FT CARBOHYD 291 291
 FT SIGNAL-REGULATORY PROTEIN BETA-1.
 FT EXTRACELLULAR (POTENTIAL).
 FT CYTOPLASMIC (POTENTIAL).
 FT IG-LIKE V-TYPE DOMAIN.
 FT IG-LIKE C1-TYPE DOMAIN.
 FT IG-LIKE C1-TYPE DOMAIN.
 FT IG-LIKE C1-TYPE DOMAIN.
 FT POTENTIAL.
 FT POTENTIAL.
 FT POTENTIAL.
 FT POTENTIAL.
 FT POTENTIAL.


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DE 01-NOV-1998 (TREMBlrel. 08, Created)
DT 01-NOV-1998 (TREMBlrel. 08, Last sequence update)
DT 01-NOV-1999 (TREMBlrel. 12, Last annotation update)
DE SURROGATE LIGHT CHAIN (FRAGMENT).
GN VPREB.
OC Bos taurus (Bovine).
OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae; Bovidae;
OC Bovinae; Bos.
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-BONE MARROW.
RA RAYCHEL A.P., HALLIGAN B.D.;
RA Submitted (MAY-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF068846; AAC19380.1; -.
DR HSSP: F01703; 7FAB.
FT NON_TER 1
FT SIGNAL 1
SO SEQUENCE 100 AA; 11142 MW; 3785537C CRC32;

Query Match
Best Local Similarity 17.6%; Score 108; DB 6; Length 100;
Matches 32; Conservative 13; Mismatches 32; Indels 10; Gaps 5;

DE 11 VMTQSPATLSVSPGERATLSCRASQSVSSNL---AWYQKRGQAPRLI--YGASPRATG 65
DB 15 VLSQPSVASF-LGATVRLACTLSSDHVNLHSITWQKRGHPRPLNLFSPSDRKQG 73
QY 66 --IPARFSGSGSGTEFT--LTISLSQS 88
DB 74 HKVPRFSGSKDLAKNTGYSLNELQA 100

RESULT 12
QY298 PRELIMINARY; PRT; 150 AA.
AC Q9Y298;
DT 01-NOV-1999 (TREMBlrel. 12, Created)
DT 01-NOV-1999 (TREMBlrel. 12, Last sequence update)
DT 01-NOV-1999 (TREMBlrel. 12, Last annotation update)
DE IGG VH PROTEIN PRECURSOR (FRAGMENT).
GN IGG VH.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Primates; Catarrhini; Homiidae; Homo.
RN [1]
RP SEQUENCE FROM N.A.
RA JACOUEMIN M.G., VANDER ELST L.P.L.;
RA EEDLINE: 98322155.
RT "Mechanism and kinetics of factor VIII inactivation: study with an
RT IgG4 monoclonal antibody derived from a hemophilia A patient with
RT inhibitor."
RL Blood 92:496-506(1998).
DR EMBL: AJ224083; CA11829.1; -.
KW Signal.
FT SIGNAL 1
FT NON_TER 150
FT POTENTIAL.
SO SEQUENCE 150 AA; 16031 MW; B18C39A CRC32;

Query Match
Best Local Similarity 17.4%; Score 107; DB 4; Length 150;
Matches 41; Conservative 18; Mismatches 43; Indels 24; Gaps 8;

QY 6 TGEIWTQSPATLSVSPGERATLSCRASQSVSSNL--WYQKRGQAPRLIYGASTRA 63
DB 17 THAQVQLVDSGAEVK-KPGASVYKSCVSGYTLTELPVHWGAPKRG--LEWVGSPDPE 73
QY 64 TG--IAR-SSGSGSGTEFTL-----ISSLSQSDFAVYVC-----QQYNNMPYTFQ 109
DB 74 SGEIYAREFGSVTWTADSTDIAYWELSLSSDDIYAVYCAVPPDARDIW----GQ 128

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QY 110 GFKLEI 115
DB 129 GIMVTV 134

RESULT 13
Q46631 PRELIMINARY; PRT; 506 AA.
AC Q46631;
DT 01-JUN-1998 (TREMBlrel. 06, Created)
DT 01-JUN-1998 (TREMBlrel. 06, Last sequence update)
DT 01-MAY-1999 (TREMBlrel. 10, Last annotation update)
DE MYD-1 ANTIGEN PRECURSOR.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae; Bovidae;
OC Bovinae; Bos.
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-PERIPHERAL BLOOD;
RX MEDLINE: 98143722.
RA BROOKE G.P., PARSONS K.R., HOWARD C.J.;
RT "Cloning of two members of the SIRP alpha family of protein tyrosine
RT phosphatase binding proteins in cattle that are expressed on monocytes
RT and a subpopulation of dendritic cells and which mediate binding to
RT CD4 T cells."
RL Eur. J. Immunol. 28:1-11(1998).
DR EMBL: Y11046; CAA1943.1; -.
DR PFAM: PF00047; 19; 3.
FT SIGNAL 1
FT CHAIN 27
FT POTENTIAL.
FT MYD-1 ANTIGEN.
SO SEQUENCE 506 AA; 55092 MW; 3D320629 CRC32;

Query Match
Best Local Similarity 17.2%; Score 105.5; DB 6; Length 506;
Matches 32; Conservative 19; Mismatches 46; Indels 27; Gaps 4;

QY 8 GEIVMTQSPATLSVSPGERATLSCRAQSQSVSSNLAM-----YQKRGQAPRL 55
DB 32 GEIVQVQIPERSVAVAGETALHCTVSLSPVGIKWFKGTGGRFIVSQKAPPRVT 91
QY 56 IYGASTRATGIPARFSGSGTEFTLISLQSDFAVYVCQYNNMP-----PYTGQGT 111
DB 92 NVSDATKRNMM-----DFSIRISNTPDADAGVYCVAFRRERGDMEKSGPGT 140
QY 112 KLEI 115
DB 141 HLTAV 144

RESULT 14
Q70153 PRELIMINARY; PRT; 228 AA.
AC Q70153;
DT 01-ANG-1998 (TREMBlrel. 07, Created)
DT 01-ANG-1998 (TREMBlrel. 07, Last sequence update)
DT 01-MAY-1999 (TREMBlrel. 10, Last annotation update)
DE B29/IG-BETA/CD79B.
GN B29/IG-BETA.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
RN [1]
RP SEQUENCE FROM N.A.
RA STRAIN-WISTAR; TISSUE-BRAIN;
RX MEDLINE: 98207252.
RA NAKAZATO S., NOMOTO K., KAZAHARI K., ONO M.;
RT "Physical linkage of the B29/Ig-beta (CD79B) gene to the skeletal
RT muscle, sodium-channel, and growth hormone genes in rat and human."
RL Genomics 48:363-368(1998).
DR EMBL: AB004831; BAA25652.1; -.

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